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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07K 14/00	A2	(11) International Publication Number: WO 98/28333 (43) International Publication Date: 2 July 1998 (02.07.98)
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(54) Title: USPA1 AND USPA2 ANTIGENS OF <i>MORAXELLA CATARRHALIS</i> (57) Abstract The present invention discloses the existence of two novel proteins UspA1 and UspA2, and their respective genes <i>uspA1</i> and <i>uspA2</i> . Each protein encompasses a region that is conserved between the two proteins and comprises an epitope that is recognized by MAb 17C7. One or more than one of these species may aggregate to form the very high molecular weight form (i.e. greater than 200 kDa) of the UspA antigen. Compositions and both diagnostic and therapeutic methods for the treatment and study of <i>M. catarrhalis</i> are disclosed.		

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DESCRIPTION

USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS

BACKGROUND OF THE INVENTION

I. Field of the Invention

5 The present invention relates generally to the fields of microbiology, and clinical bacteriology. More particularly, it concerns sequences of the *uspA1* and *uspA2* genes which encode the proteins UspA1 and UspA2, respectively, both of which encode an epitope reactive with monoclonal antibody (MAb) 17C7 and provide useful epitopes for immunodiagnosis and immunoprophylaxis.

II. Description of Related Art

10 It was previously thought that *Moraxella catarrhalis*, previously known as *Branhamella catarrhalis* or *Neisseria catarrhalis*, was a harmless saprophyte of the upper respiratory tract (Catlin, 1990; Berk, 1990). However, during the previous decade, it has been determined that
15 this organism is an important human pathogen. Indeed, it has been established that this Gram-negative diplococcus is the cause of a number of human infections (Murphy, 1989). *M. catarrhalis* is now known to be the third most common cause of both acute and chronic otitis media (Catlin, 1990; Faden *et al.*, 1990; 1991; Marchant, 1990), the most common disease for which infants and children receive health care according to the 1989 Consensus Report. This
20 organism also causes acute maxillary sinusitis, generalized infections of the lower respiratory tract (Murphy and Loeb, 1989) and is an important cause of bronchopulmonary infections in patients with underlying chronic lung disease and, less frequently, of systemic infections in immunocompromised patients (Melendez and Johnson, 1990; Sarubbi *et al.*, 1990; Schonheyder and Ejertsen, 1989; Wright and Wallace, 1989).

25 The 1989 Consensus Report further concluded that prevention of otitis media is an important health care goal due to both its occurrence in infants and children, as well as certain populations of all age groups. In fact, the total financial burden of otitis media has been estimated to be at least \$2.5 billion annually. Vaccines were identified as the most desired approach to prevent this disease for a number of reasons. For example, it was estimated that if

vaccines could reduce the incidence of otitis media by 30%, then the annual health care savings would be at least \$400 million. However, while some progress has been made in the development of vaccines for 2 of the 3 common otitis media pathogens, *Streptococcus pneumoniae* and *Haemophilus influenzae*, there is no indication that similar progress has been made with respect to *M. catarrhalis*. This is particularly troublesome in that *M. catarrhalis* now accounts for approximately 17-20% of all otitis media infection (Murphy, 1989). In addition, *M. catarrhalis* is also a significant cause of sinusitis (van Cauwenberge *et al.*, 1993) and persistent cough (Gottfarb and Brauner, 1994) in children. In the elderly, it infects patients with predisposing conditions such as chronic obstructive pulmonary disease (COPD) and other chronic cardiopulmonary conditions (Boyle *et al.*, 1991; Davies and Maesen, 1988; Hager *et al.*, 1987).

Despite its recognized virulence potential, little is known about the mechanisms employed by *M. catarrhalis* in the production of disease or about host factors governing immunity to this pathogen. An antibody response to *M. catarrhalis* otitis media has been documented by means of an ELISA system using whole *M. catarrhalis* cells as antigen and acute and convalescent sera or middle ear fluid as the source of antibody (Leinonen *et al.*, 1981). The development of serum bactericidal antibody during *M. catarrhalis* infection in adults was shown to be dependent on the classical complement pathway (Chapman *et al.*, 1985). And more recently, it was reported that young children with *M. catarrhalis* otitis media develop an antibody response in the middle ear but fail to develop a systemic antibody response in a uniform manner (Faden *et al.*, 1992).

Previous attempts have been made to identify and characterize *M. catarrhalis* antigens that would serve as potentially important targets of the human immune response to infection (Murphy, 1989; Goldblatt *et al.*, 1990; Murphy *et al.*, 1990). Generally speaking, the surface of *M. catarrhalis* is composed of outer membrane proteins (OMPs), lipooligosaccharide (LOS) and fimbriae. *M. catarrhalis* appears to be somewhat distinct from other Gram-negative bacteria in that attempts to isolate the outer membrane of this organism using detergent fractionation of cell envelopes has generally proven to be unsuccessful in that the procedures did not yield consistent results (Murphy, 1989; Murphy and Loeb, 1989). Moreover, preparations were found to be contaminated with cytoplasmic membranes, suggesting an unusual characteristic of the *M. catarrhalis* cell envelope.

Passive immunization with polyclonal antisera raised against outer membrane vesicles of the *M. catarrhalis* strain 035E was also found to protect against pulmonary challenge by the heterologous *M. catarrhalis* strain TTA24. In addition, active immunization with *M. catarrhalis* outer membrane vesicles resulted in enhanced clearance of this organism from the lungs after challenge. The positive effect of immunization in pulmonary clearance indicates that antibodies play a major role in immunoprotection from this pathogen. In addition, the protection observed against pulmonary challenge with a heterologous *M. catarrhalis* strain demonstrates that one or more conserved surface antigens are targets for antibodies which function to enhance clearance of *M. catarrhalis* from the lungs.

Outer membrane proteins (OMPs) constitute major antigenic determinants of this unencapsulated organism (Bartos and Murphy, 1988) and different strains share remarkably similar OMP profiles (Bartos and Murphy, 1988; Murphy and Bartos, 1989). At least three different surface-exposed outer membrane antigens have been shown to be well-conserved among *M. catarrhalis* strains; these include the 81 kDa CopB OMP (Helminen *et al.*, 1993b), the heat-modifiable CD OMP (Murphy *et al.*, 1993) and the high-molecular weight UspA antigen (Helminen *et al.*, 1994). Of these three antigens, both the CopB protein and UspA antigen have been shown to bind antibodies which exert biological activity against *M. catarrhalis* in an animal model (Helminen *et al.*, 1994; Murphy *et al.*, 1993).

The MAb, designated 17C7, was described as binding to UspA, a very high molecular weight protein that migrated with an apparent molecular weight (in SDS-PAGE) of at least 250 kDa (Helminen *et al.*, 1994; Klingman and Murphy, 1994). MAb 17C7 enhanced pulmonary clearance of *M. catarrhalis* from the lungs of mice when used in passive immunization studies and, in colony blot radioimmunoassay analysis, bound to every isolate of *M. catarrhalis* examined. This same MAb also reacted, although less intensely, with another antigen band of approximately 100 kDa, as described in U.S. Patent No. 5,552,146 (incorporated herein by reference). A recombinant bacteriophage that contained a fragment of *M. catarrhalis* chromosomal DNA that expressed a protein product that bound MAb 17C7 was also identified and migrated at a rate similar or indistinguishable from that of the native UspA antigen from *M. catarrhalis* (Helminen *et al.*, 1994).

With the rising importance of this pathogen in respiratory tract infections, identification of the surface components of this bacterium involved in virulence expression and immunity is becoming more important. To date, there are no vaccines available, against any other OMP, LOS or fimbriae, that induce protective antibodies against *M. catarrhalis*. Thus, it is clear that there remains a need to identify and characterize useful antigens and which can be employed in the preparation of immunoprophylactic reagents. Additionally, once such an antigen or antigens is identified, there is a need for providing methods and compositions which will allow the preparation of vaccines and in quantities that will allow their use on a wide scale basis in prophylactic protocols.

SUMMARY OF THE INVENTION

It is, therefore, an object of the present invention to provide new UspA1 and UspA2 proteins and genes coding therefor. It also is an object of the present invention to provide methods of using these new proteins, for example, in the preparation of agents for the treatment and inhibition of *M. catarrhalis* infection. It also is contemplated that through the use of other technologies such as antibody treatment and immunoprophylaxis that one can inhibit or even prevent *M. catarrhalis* infections.

In satisfying these goals, there are provided epitopic core sequences of UspA1 and UspA2 which can serve as the basis for the preparation of therapeutic or prophylactic compositions or vaccines which comprise peptides of 7, 10, 20, 30, 40, 50 or even 60 amino acids in length that elicit an antigenic reaction and a pharmaceutically acceptable buffer or diluent. These peptides may be coupled to a carrier, adjuvant, another peptide or other molecule such that an effective antigenic response to *M. catarrhalis* is retained or even enhanced. Alternatively, these peptides may act as carriers themselves when coupled to another peptide or other molecule that elicits an antigenic response to *M. catarrhalis* or another pathogen. For example, UspA2 can serve as a carrier for an oligosaccharide.

In one embodiment, the epitopic core sequences of UspA1 and UspA2 comprise one or more isolated peptides of 7, 10, 20, 30, 40, 50 or even 60 amino acids in length having the amino acid sequence AQQQDQH (SEQ ID NO:17).

In another embodiment, there are provided nucleic acids, *uspA1* and *uspA2*, which encode the UspA1 and the UspA2 antigens, respectively, as well as the amino acid sequences of the UspA1 and UspA2 antigens of the *M. catarrhalis* isolates O35E, TTA24, TTA37, and O46E. It is envisioned that nucleic acid segments and fragments of the genes *uspA1* and *uspA2* and the UspA1 and UspA2 antigens will be of value in the preparation and use of therapeutic or prophylactic compositions or vaccines for treating, inhibiting or even preventing *M. catarrhalis* infections.

In another embodiment, there is provided a method for inducing an immune response in a mammal comprising the step of providing to the mammal an antigenic composition that comprises an isolated peptide of about 20 to about 60 amino acids that contains the identified epitopic core sequence and a pharmaceutically acceptable buffer or diluent.

In another embodiment, there is provided a method for diagnosing *M. catarrhalis* infection which comprises the step of determining the presence, in a sample, of an *M. catarrhalis* amino acid sequence corresponding to residues of the epitopic core sequences of either the UspA1 or UspA2 antigen. This method may comprise PCR™ detection of the nucleotide sequences or alternatively an immunologic reactivity of an antibody to either a UspA1 or UspA2 antigen.

In a further embodiment, there is provided a method for treating an individual having an *M. catarrhalis* infection which comprises providing to the individual an isolated peptide of about 20 to about 60 amino acids that comprises at least about 10 consecutive residues of the amino acid sequence identified as an epitopic core sequence of UspA1 or UspA2.

In a still further embodiment, there is provided a method for preventing or limiting an *M. catarrhalis* infection that comprises providing to a subject an antibody that reacts immunologically with the identified epitopic core region of either UspA1 or UspA2 of *M. catarrhalis*.

In another embodiment, there is provided a method for screening a peptide for reactivity with an antibody that binds immunologically to UspA1, UspA2 or both which comprises the steps of providing the peptide and contacting the peptide with the antibody and then

determining the binding of the antibody to the peptide. This method may comprise an immunoassay such as a western blot, an ELISA, an RIA or an immunoaffinity separation.

In a still further embodiment, there is provided a method for screening a UspA1 or UspA2 peptide for its ability to induce a protective immune response against *M. catarrhalis* by providing the peptide, administering it in a suitable form to an experimental animal, challenging the animal with *M. catarrhalis* and then assaying for an *M. catarrhalis* infection in the animal. It is envisioned that the animal used will be a mouse that is challenged by a pulmonary exposure to *M. catarrhalis* and that the assaying comprises assessing the degree of pulmonary clearance by the mouse.

Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating preferred embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

FIG. 1. Southern blot analysis of *Pvu*II-digested chromosomal DNA from strains of *M. catarrhalis* using a probe from the *uspA1* gene. Bacterial strain designations are at the top; kilobase (kb) position markers are on the left.

FIG. 2A. Proteins present in whole cell lysates of the wild-type strain O35E and the isogenic *uspA1* mutant strain. These proteins were resolved by SDS-PAGE and stained with Coomassie blue. The left lane (WT) contains the wild-type strain and right lane (MUT) contains

the mutant. The arrows indicate the protein, approximately 120 kDa in size, that is present in the wild-type and missing in the mutant. Kilodalton position markers are on the left.

FIG. 2B. Western blot analysis of whole cell lysates of the wild-type strain O35E and the isogenic *uspA1* mutant strain. These proteins were resolved by SDS-PAGE and probed with MAb 17C7 in western blot analysis. The left lane (WT) contains the wild-type strain and the right lane (MUT) contains the mutant. Kilodalton position markers are on the left. It can be seen that both strains possess the very high molecular weight band reactive with MAb 17C7 whereas only the wild-type strain also has a band of approximately 120 kDa that binds this MAb.

FIG. 2C. Western blot analysis of whole cell lysate (WCL) and EDTA-extracted outer membrane vesicles (OMV) from the wild-type strain O35E (WT) and the isogenic *uspA1* mutant (MUT) using MAb 17C7. Samples were either heated at 37°C for 15 minutes (H) or at 100°C for 5 minutes (B) prior to SDS-PAGE. Molecular weight position markers (in kilodaltons) are indicated on the left. The open arrow indicates the position of the very high molecular weight form of the MAb 17C7-reactive antigen; the closed arrow indicates the position of the approximately 120 kDa protein; the open circle indicates the position of the approximately 70-80 kDa protein.

FIG. 3. Southern blot analysis of chromosomal DNA from the wild-type *M. catarrhalis* strain O35E and the isogenic *uspA1* mutant. Chromosomal DNA was digested with *PvuII* and probed with a 0.6 kb *BglII-PvuII* fragment from the *uspA1* gene. The wild-type strain is listed as O35E at the top of this figure and the mutant strain is listed as O35E-*uspA1*⁻. Kilobase position markers are present on the left side.

FIG. 4. Western blot reactivity of proteins in *M. catarrhalis* strain O35E outer membrane vesicles (labeled O35E OMV) and the MF-4-1 GST fusion protein (labeled GST fusion protein) with MAb 17C7.

FIG. 5. PCRTM products obtained by the use of the T3 and P10 primers (middle lane - 0.9 kb product) and the T7 and P9 primers (right lane - 1.7 kb product) when used in a PCRTM

amplification with chromosomal DNA from the *uspA1* mutant. A kb ladder is present in the first lane; several kb position markers are listed on the left side of this figure.

FIG. 6A-6C. SDS-PAGE and westerns of purified proteins. FIG. 6A. Coomassie blue stained gel of purified UspA2 (lane 2). FIG. 6B. Coomassie blue stained gel of purified UspA1 prepared without heating of sample (lane 4), heated for 3 min at 100°C (lane 5), heated for 5 min at 100°C (lane 6), and heated for 10 min at 100°C (lane 7). FIG. 6C. Western of the purified UspA2 (lane 9) and purified UspA1 (lane 10) probed with the 17C7 MAb. Both proteins were heated 10 min. The molecular size markers in lanes 1, 3, and 8 are as indicated in kilodaltons.

FIG. 7. Interaction of purified UspA1 and UspA2 with HEp-2 cells as determined by ELISA. HEp-2 cell monolayers cultured in 96-well plate were incubated with serially diluted UspA1 or UspA2. O35E bacterial strain was used as the positive control. The bacteria were diluted analogous to the proteins beginning with a suspension with an A_{550} of 1.0. The bound proteins or attached bacteria were detected with a 1:1 mixed antisera to UspA1 and UspA2 as described in the methods.

FIG. 8. Interaction with fibronectin and vitronectin determined by dot blot. The bound vitronectin was detected with rabbit polyclonal antibodies, the protein bound to the fibronectin was detected with pooled sera made against the UspA1 and UspA2.

FIG. 9. The levels of antibodies to the protein UspA1, UspA2 and *M. catarrhalis* O35E strain in normal human sera. Data are the \log_{10} transformed end-point titers of the IgG (FIGs. 9A-9C) and IgA (FIGs. 9D-9F) antibodies determined by ELISA. The individual titers were plotted according to age group and the geometric mean titer for each age group linked by a solid line. Sera for the 2-18 month old children were consecutive samples from a group of ten children.

FIG. 10. Subclass distribution of IgG antibodies to UspA1 and UspA2 in normal human sera. FIG. 10A shows titers toward UspA1 and FIG. 10B shows titers to UspA2.

FIG. 11. Relationship of serum IgG titers to UspA1 (FIG. 11A) and UspA2 (FIG. 11B) with the bactericidal titer against the O35E strain determined by logistic regression ($p < 0.05$). The solid line indicates the linear relationship between the IgG titer and bactericidal titer. Broken lines represent the 95 % confidence intervals of the linear fit.

FIG. 12. Schematic drawing showing the relative positions of decapeptides 10-24 within the region of UspA1 and UspA2 which binds to MAb 17C7.

FIG. 13. Western dot blot analysis demonstrating reactivity of decapeptides 10-24 with MAb 17C7.

FIG. 14. Partial restriction enzyme map of the *uspA1* (FIG. 14A) and *uspA2* (FIG. 14B) genes from *M. catarrhalis* strain O35E and the mutated versions of these genes. The shaded boxes indicate the open reading frame of each gene. Relevant restriction sites are indicated. PCRTM primer sites (P1-P6) are indicated by arrows. The DNA fragments containing the partial *uspA1* and *uspA2* open reading frames that were derived from *M. catarrhalis* strain O35E chromosomal DNA by PCRTM and cloned into pBluescriptII SK+ are indicated by black bars. Dotted lines connect corresponding restriction sites on these DNA inserts and the chromosome. Open bars indicate the location of the kanamycin or chloramphenicol cassettes, respectively. The DNA probes specific for *uspA1* or *uspA2* are indicated by the appropriate cross-hatched bars and were amplified by PCRTM from *M. catarrhalis* strain O35E chromosomal DNA by the use of the oligonucleotide primer pairs

P3 (5'-GACGCTCAACAGCACTAATACG-3') (SEQ ID NO:20)/P4
(5'-CCAAGCTGATATCACTACC-3') (SEQ ID NO:21) and
P5 (5'-TCAATGCCTTTGATGGTC-3') (SEQ ID NO:22)/P6
(5'-TGTATGCCGCTACTCGCAGCT-3') (SEQ ID NO:23), respectively.

FIG. 15. Detection of the UspA1 and UspA2 proteins in wild-type and mutant strains of *M. catarrhalis* O35E. Proteins present in EDTA-extracted outer membrane vesicles from the wild-type strain (lane 1), the *uspA1* mutant strain O35E.1 (lane 2), the *uspA2* mutant strain O35E.2 (lane 3), and the isogenic *uspA1 uspA2* double mutant strain O35E.12 (lane 4) were resolved by SDS-PAGE, and either stained with Coomassie blue (FIG. 15A) or transferred to nitrocellulose and probed with MAb 17C7 followed by radioiodinated goat anti-mouse

immunoglobulin in western blot analysis. In FIG. 15A, the closed arrow indicates the very high molecular weight form of the UspA antigen which is comprised of both UspA1 and UspA2. In FIG. 15B, the bracket on the left indicates the very high molecular weight forms of the UspA1 and UspA2 proteins that bind MAb 17C7. The open arrow indicates the 120 kDa, putative monomeric form of UspA1. The closed arrow indicates the 85 kDa, putative monomeric form of UspA2. Molecular weight position markers (in kilodaltons) are present on the left.

FIG. 16. Comparison of the rate and extent of growth of the wild-type and mutant strains of *M. catarrhalis*. The wild-type strain O35E (closed squares), the *uspA1* mutant O35E.1 (open squares), the *uspA2* mutant O35E.2 (closed circles), and the *uspA1 uspA2* double mutant O35E.12 (open circles) of *M. catarrhalis* O35E from overnight broth cultures were diluted to a density of 35 Klett units in BHI broth and subsequently allowed to grow at 37° with shaking. Growth was followed by means of turbidity measurements.

FIG. 17. Susceptibility of wild-type and mutant strains of *M. catarrhalis* to killing by normal human serum. Cells of the wild-type parent strain O35E (diamonds), *uspA1* mutant O35E.1 (triangles), *uspA2* mutant O35E.2 (circles), and *uspA1 uspA2* double mutant O35E.12 (squares) from logarithmic-phase BHI broth cultures were incubated in the presence of 10% (v/v) normal human serum (closed symbols) or heat-inactivated normal human serum (open symbols). Data are presented as the percentage of the original inoculum remaining at each time point.

DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

The present invention relates to the identification of epitopes useful for developing potential vaccines against *M. catarrhalis*. Early work was directed at determining the molecular nature of the UspA antigen and characterize the epitope which is recognized by the MAb 17C7. Preliminary work indicated that MAb 17C7 recognizes a single antigenic epitope and it was believed that this epitope was encoded by a single gene. However, isolation of the protein which contained the epitope yielded unexpected results. MAb 17C7 recognized a single epitope, but the characteristics of the protein associated with the epitope suggested the existence

of not one but two separate proteins. Further careful analyses led to a surprising discovery. A single epitope of the UspA antigen is recognized by the MAb 17C7, but this epitope is present in two different proteins, UspA1 and UspA2, which are encoded by two different genes *uspA1* and *uspA2*, respectively, and only have 43% identity to each other. The present invention provides the nucleotide sequences of the genes *uspA1* and *uspA2*, their respective protein products, UspA1 and UspA2, and the shared epitope recognized by MAb 17C7.

In addition, the present invention provides insights into the antigenic structure of the UspA protein based on the analysis of the sequences of the UspA1 and UspA2 proteins which comprise the protein. Characterization of the epitopic region of the molecule that is targeted by the MAb 17C7 permits the development of agents that will be useful in protecting against *M. catarrhalis* infections, e.g., in the preparation of prophylactic reagents. Particular embodiments relate to the amino acid and nucleic acids corresponding to the UspA1 and UspA2 proteins, peptides and antigenic compositions derived therefrom, and methods for the diagnosis and treatment of *M. catarrhalis* disease.

As stated previously, *M. catarrhalis* infections present a serious health challenge, especially to the young. Thus, there is a clear need to develop compositions and methods that will aid in the treatment and diagnosis of this disease. The present invention, by virtue of new information regarding the structure of the UspA antigen of *M. catarrhalis*, and discovery of the two new and distinct proteins UspA1 and UspA2 provides such improved compositions and methods. UspA1 and UspA2 represent important antigenic determinants, as the MAb 17C7 has been shown to protect experimental animals, as measured in a pulmonary clearance model, when provided in passive immunizations.

In a first embodiment, the present invention provides for the identification of the proteins UspA1 and UspA2 from *M. catarrhalis* strain O35E. The UspA1 protein comprises about 831 amino acid residues and has a predicted mass of about 88,271 daltons (SEQ ID NO:1). The UspA2 protein comprises about 576 residues and has a predicted mass of about 62,483 daltons (SEQ ID NO:3). UspA2 is not a truncated or processed form of UspA1.

In a second embodiment, the present invention has identified the specific epitope to which MAb 17C7 binds. A common peptide sequence, designated as the "3Q" peptide, found between amino acid residues 480-502 and 582-604 of the UspA1 protein (SEQ ID NO:1) and

residues 355-377 of the UspA2 protein (SEQ ID NO:3) of *M. catarrhalis* strain 035E, encompasses the region which appears to be recognized by MAb 17C7. (Note that numbering of the amino acid residues is based upon strain O35E as provided in SEQ ID NO:3.) It is envisioned that this region plays an important role in the biology of the pathogen and, from this information, one will deduce amino acids residues that are critical in MAb 17C7 antibody binding. It also is envisioned that, based upon this information, one will be able to design epitopic regions that have either a higher or lower affinity for the MAb 17C7 or other antibodies. Further embodiments of the present invention are discussed below.

In another preferred embodiment, the present invention provides DNA segments, vectors and the like comprising at least one isolated gene, DNA segment or coding region that encodes a *M. catarrhalis* UspA1 or UspA2 protein, polypeptide, domain, peptide or any fusion protein thereof. Herein are provided at least an isolated gene, DNA segment or coding region that encodes a *M. catarrhalis uspA1* gene comprising about 2493 base pairs (bp) (SEQ ID NO:2) of strain O35E, about 3381 bp (SEQ ID NO:6) of strain O46E, about 3538 bp (SEQ ID NO:10) of strain TTA24, or about 3292 bp (SEQ ID NO:14) of strain TTA37. Further provided are at least an isolated gene, DNA segment or coding region that encodes a *M. catarrhalis uspA2* gene comprising about 1728 bp (SEQ ID NO:4) of strain O35E, about 3295 bp (SEQ ID NO:8) of strain O46E, about 2673 bp (SEQ ID NO:12), or about 4228 bp (SEQ ID NO:16) of strain TTA37. It is envisioned that the *uspA1* and *uspA2* genes will be useful in the preparation of proteins, antibodies, screening assays for potential candidate drugs and the like to treat or inhibit, or even prevent, *M. catarrhalis* infections.

The present invention also provides for the use of the UspA1 or UspA2 proteins or peptides as immunogenic carriers of other agents which are useful for the treatment, inhibition or even prevention of other bacterial, viral or parasitic infections. It is envisioned that either the UspA1 or UspA2 antigen, or portions thereof, will be coupled, bonded, bound, conjugated or chemically-linked to one or more agents via linkers, polylinkers or derivatized amino acids such that a bispecific or multivalent composition or vaccine which is useful for the treatment, inhibition or even prevention of infection by *M. catarrhalis* and another pathogen(s) is prepared. It is further envisioned that the methods used in the preparation of these compositions will be familiar to those of skill in the art and, for example, similar to those used to prepare conjugates to keyhole limpet hemocyanin (KLH) or bovine serum albumin (BSA).

It is important to note that screening methods for diagnosis and prophylaxis are readily available, as set forth below. Thus, the ability to (i) test peptides, mutant peptides and antibodies for their reactivity with each other and (ii) test peptides and antibodies for the ability to prevent infections *in vivo*, provide powerful tools to develop clinically important reagents.

1.0 UspA Proteins, Peptides and Polypeptides

The present invention, in one embodiment, encompasses the two new protein sequences, UspA1 and UspA2, and the peptide sequence AQQQDQH (SEQ ID NO:17) identified as the target epitope of Mab 17C7. In addition, inspection of the amino acid sequences of the UspA1 and UspA2 proteins from four strains of *M. catarrhalis* indicated that each protein contained at least one copy of the peptide YELAQQQDQH (SEQ ID NO:18) which binds Mab 17C7 or, in one instance, a peptide nearly identical and having the amino acid sequence YDLAQQQDQH (SEQ ID NO:19).

The peptide (YELAQQQDQH, SEQ ID NO:18) occurs twice in UspA1 from strain O35E at residues 486-495 and 588-597 (SEQ ID NO:1) and once in UspA2 from strain O35E at residues 358-367 (SEQ ID NO:3). It occurs once in UspA1 from strain TTA24 at residues 497-506 (SEQ ID NO:9) and twice in UspA2 from strain TTA24 at residues 225-234 and 413-422 (SEQ ID NO:11). The peptide YDLAQQQDQH (SEQ ID NO:19) occurs once in UspA1 from strain O46E at residues 448-457 (SEQ ID NO:5) whereas the peptide YELAQQQDQH (SEQ ID NO:18) occurs once in this same protein at residues 649-658 (SEQ ID NO:5). The peptide YELAQQQDQH (SEQ ID NO:18) occurs once in UspA2 from strain O46E at residues 416-425 (SEQ ID NO:7). The peptide YELAQQQDQH (SEQ ID NO:18) occurs twice in UspA1 from strain TTA37 at residues 478-487 and 630-639 (SEQ ID NO:13) and twice in UspA2 from strain TTA37 at residues 522-531 and 681-690 (SEQ ID NO:15).

Also encompassed in the present invention are hybrid molecules containing portions from one UspA protein, for example the UspA1 protein, fused with portions of the other UspA protein, in this example the UspA2 protein, or fused with other proteins which are useful for identification, such as kanamycin-resistance, or other purposes in the screening of potential vaccines or further characterization of the UspA1 and UspA2 proteins. For example, one may fuse residues 1-350 of any UspA1 with residues 351-576 of any UspA2. Alternatively, a fusion could be generated with sequences from three, four or even five peptide regions represented in a

single UspA antigen. Also encompassed are fragments of the disclosed UspA1 and UspA2 molecules, as well as insertion, deletion or replacement mutants in which non-UspA sequences are introduced, UspA sequences are removed, or UspA sequences are replaced with non-UspA sequences, respectively.

5 UspA1 and UspA2 proteins, according to the present invention, may be advantageously cleaved into fragments for use in further structural or functional analysis, or in the generation of reagents such as UspA-related polypeptides and UspA-specific antibodies. This can be accomplished by treating purified or unpurified UspA1 and/or UspA2 with a peptidase such as endoproteinase glu-C (Boehringer, Indianapolis, IN). Treatment with CNBr is another method by
10 which UspA1 and/or UspA2 fragments may be produced from their natural respective proteins. Recombinant techniques also can be used to produce specific fragments of UspA1 or UspA2.

15 More subtle modifications and changes may be made in the structure of the encoded UspA1 or UspA2 polypeptides of the present invention and still obtain a molecule that encodes a protein or peptide with characteristics of the natural UspA antigen. The following is a discussion based upon changing the amino acids of a protein to create an equivalent, or even an improved, second-generation molecule. The amino acid changes may be achieved by changing the codons of the DNA sequence, according to the following codon table:

TABLE I

Amino acid names and abbreviations			Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	UGC	UGU					
Aspartic acid	Asp	D	GAC	GAU					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	UUC	UUU					
Glycine	Gly	G	GGA	GGC	GGG	GGU			
Histidine	His	H	CAC	CAU					
Isoleucine	Ile	I	AUA	AUC	AUU				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU	
Methionine	Met	M	AUG						
Asparagine	Asn	N	AAC	AAU					
Proline	Pro	P	CCA	CCC	CCG	CCU			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU	
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU	
Threonine	Thr	T	ACA	ACC	ACG	ACU			
Valine	Val	V	GUA	GUC	GUG	GUU			
Tryptophan	Trp	W	UGG						
Tyrosine	Tyr	Y	UAC	UAU					

It is known that certain amino acids may be substituted for other amino acids in a protein structure in order to modify or improve its antigenic or immunogenic activity (see, *e.g.*,
 5 Kyte & Doolittle, 1982; Hopp, U.S. patent 4,554,101, incorporated herein by reference). For example, through the substitution of alternative amino acids, small conformational changes may

be conferred upon a polypeptide which result in increased activity or stability. Alternatively, amino acid substitutions in certain polypeptides may be utilized to provide residues which may then be linked to other molecules to provide peptide-molecule conjugates which retain enough antigenicity of the starting peptide to be useful for other purposes. For example, a selected UspA1 or UspA2 peptide bound to a solid support might be constructed which would have particular advantages in diagnostic embodiments.

The importance of the hydropathic index of amino acids in conferring interactive biological function on a protein has been discussed generally by Kyte & Doolittle (1982), wherein it is found that certain amino acids may be substituted for other amino acids having a similar hydropathic index or core and still retain a similar biological activity. As displayed in Table II below, amino acids are assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics. It is believed that the relative hydropathic character of the amino acid determines the secondary structure of the resultant protein, which in turn defines the interaction of the protein with substrate molecules. Preferred substitutions which result in an antigenically equivalent peptide or protein will generally involve amino acids having index scores within ± 2 units of one another, and more preferably within ± 1 unit, and even more preferably, within ± 0.5 units.

TABLE II

Amino Acid	Hydropathic Index
Isoleucine	4.5
Valine	4.2
Leucine	3.8
Phenylalanine	2.8
Cysteine/cystine	2.5
Methionine	1.9
Alanine	1.8
Glycine	-0.4
Threonine	-0.7

Table II (Continued)

Amino Acid	Hydropathic Index
Tryptophan	-0.9
Serine	-0.8
Tyrosine	-1.3
Proline	-1.6
Histidine	-3.2
Glutamic Acid	-3.5
Glutamine	-3.5
Aspartic Acid	-3.5
Asparagine	-3.5
Lysine	-3.9
Arginine	-4.5

Thus, for example, isoleucine, which has a hydropathic index of +4.5, will preferably be exchanged with an amino acid such as valine (+ 4.2) or leucine (+ 3.8). Alternatively, at the other end of the scale, lysine (- 3.9) will preferably be substituted for arginine (-4.5), and so on.

Substitution of like amino acids may also be made on the basis of hydrophilicity, particularly where the biological functional equivalent protein or peptide thereby created is intended for use in immunological embodiments. U.S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, *i.e.* with an important biological property of the protein.

As detailed in U.S. Patent 4,554,101, each amino acid has also been assigned a hydrophilicity value. These values are detailed below in Table III.

TABLE III

Amino Acid	Hydrophilic Index
arginine	+3.0
lysine	+3.0
aspartate	+3.0 \pm 1
glutamate	+3.0 \pm 1
serine	+0.3
asparagine	+0.2
glutamine	+0.2
glycine	0
threonine	-0.4
alanine	-0.5
histidine	-0.5
proline	-0.5 \pm 1
cysteine	-1.0
methionine	-1.3
valine	-1.5
leucine	-1.8
isoleucine	-1.8
tyrosine	-2.3
phenylalanine	-2.5
tryptophan	-3.4

It is understood that one amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those which are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

Accordingly, these amino acid substitutions are generally based on the relative similarity of R-group substituents, for example, in terms of size, electrophilic character, charge, and the like. In general, preferred substitutions which take various of the foregoing characteristics into

consideration will be known to those of skill in the art and include, for example, the following combinations: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, peptides derived from these polypeptides, including peptides of at least about 6 consecutive amino acids from these sequences, are contemplated. Alternatively, such peptides may comprise about 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59 or 60 consecutive residues. For example, a peptide that comprises 6 consecutive amino acid residues may comprise residues 1 to 6, 2 to 7, 3 to 8 and so on of the UspA1 or UspA2 protein. Such peptides may be represented by the formula

$$x \text{ to } (x + n) = 5' \text{ to } 3' \text{ the positions of the first and last consecutive residues}$$

where x is equal to any number from 1 to the full length of a UspA1 or UspA2 protein and n is equal to the length of the peptide minus 1. So, for UspA1, $x = 1$ to 831, for UspA2, $x = 1$ to 576. Where the peptide is 10 residues long ($n = 10 - 1$), the formula represents every 10-mer possible for each antigen. For example, where x is equal to 1 the peptide would comprise residues 1 to $(1 + [10 - 1])$, or 1 to 10. Where x is equal to 2, the peptide would comprise residues 2 to $(2 + [10 - 2])$, or 2 to 11, and so on.

Syntheses of peptides are readily achieved using conventional synthetic techniques such as the solid phase method (*e.g.*, through the use of a commercially available peptide synthesizer such as an Applied Biosystems Model 430A Peptide Synthesizer). Peptides synthesized in this manner may then be aliquoted in predetermined amounts and stored in conventional manners, such as in aqueous solutions or, even more preferably, in a powder or lyophilized state pending use.

In general, due to the relative stability of peptides, they may be readily stored in aqueous solutions for fairly long periods of time if desired, *e.g.* up to six months or more, in virtually any aqueous solution without appreciable degradation or loss of antigenic activity. However, where extended aqueous storage is contemplated it will generally be desirable to include agents including buffers such as Tris or phosphate buffers to maintain a pH of 7.0 to 7.5. Moreover, it may be desirable to include agents which will inhibit microbial growth, such as sodium azide or

Merthiolate. For extended storage in an aqueous state it will be desirable to store the solutions at 4°C, or more preferably, frozen. Of course, where the peptide(s) are stored in a lyophilized or powdered state, they may be stored virtually indefinitely, *e.g.* in metered aliquots that may be rehydrated with a predetermined amount of water (preferably distilled, deionized) or buffer prior to use.

Of particular interest are peptides that represent epitopes that lie within the UspA antigen and are encompassed by the UspA1 and UspA2 proteins of the present invention. An "epitope" is a region of a molecule that stimulates a response from a T-cell or B-cell, and hence, elicits an immune response from these cells. An epitopic core sequence, as used herein, is a relatively short stretch of amino acids that is structurally "complementary" to, and therefore will bind to, binding sites on antibodies or T-cell receptors. It will be understood that, in the context of the present disclosure, the term "complementary" refers to amino acids or peptides that exhibit an attractive force towards each other. Thus, certain epitopic core sequences of the present invention may be operationally defined in terms of their ability to compete with or perhaps displace the binding of the corresponding UspA antigen to the corresponding UspA-directed antisera.

The identification of epitopic core sequences is known to those of skill in the art. For example U.S. Patent 4,554,101 teaches identification and preparation of epitopes from amino acid sequences on the basis of hydrophilicity, and by Chou-Fasman analyses. Numerous computer programs are available for use in predicting antigenic portions of proteins, examples of which include those programs based upon Jameson-Wolf analyses (Jameson and Wolf, 1988; Wolf *et al.*, 1988), the program PepPlot® (Brutlag *et al.*, 1990; Weinberger *et al.*, 1985), and other new programs for protein tertiary structure prediction (Fetrow & Bryant, 1993) that can be used in conjunction with computerized peptide sequence analysis programs.

In general, the size of the polypeptide antigen is not believed to be particularly crucial, so long as it is at least large enough to carry the identified core sequence or sequences. The smallest useful core sequence anticipated by the present disclosure would be on the order of about 6 amino acids in length. Thus, this size will generally correspond to the smallest peptide antigens prepared in accordance with the invention. However, the size of the antigen may be larger where desired, so long as it contains a basic epitopic core sequence.

2.0 UspA1 and UspA2 Nucleic Acids

In addition to polypeptides, the present invention also encompasses nucleic acids encoding the UspA1 (SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10 and SEQ ID NO:14) and UspA2 (SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12 and SEQ ID NO:16) proteins from the exemplary *M. catarrhalis* strains O35E, O46E, TTA24 and TTA37, respectively. Because of the degeneracy of the genetic code, many other nucleic acids also may encode a given UspA1 or UspA2 protein. For example, four different three-base codons encode the amino acids alanine, glycine, proline, threonine and valine, while six different codons encode arginine, leucine and serine. Only methionine and tryptophan are encoded by a single codon. Table I provides a list of amino acids and their corresponding codons for use in such embodiments. In order to generate any nucleic acid encoding UspA1 or UspA2, one need only refer to the codon table provided herein. Substitution of the natural codon with any codon encoding the same amino acid will result in a distinct nucleic acid that encodes UspA1 or UspA2. As a practical matter, this can be accomplished by site-directed mutagenesis of an existing *uspA1* or *uspA2* gene or *de novo* chemical synthesis of one or more nucleic acids.

These observations regarding codon selection, site-directed mutagenesis and chemical synthesis apply with equal force to the discussion of substitutional mutant UspA1 or UspA2 peptides and polypeptides, as set forth above. More specifically, substitutional mutants generated by site-directed changes in the nucleic acid sequence that are designed to alter one or more codons of a given polypeptide or epitope may provide a more convenient way of generating large numbers of mutants in a rapid fashion. The nucleic acids of the present invention provide for a simple way to generate fragments (*e.g.*, truncations) of UspA1 or UspA2, UspA1-UspA2 fusion molecules (discussed above) and UspA1 or UspA2 fusions with other molecules. For example, utilization of restriction enzymes and nuclease in the *uspA1* or *uspA2* gene permits one to manipulate the structure of these genes, and the resulting gene products.

The nucleic acid sequence information provided by the present disclosure also allows for the preparation of relatively short DNA (or RNA) sequences that have the ability to specifically hybridize to gene sequences of the selected *uspA1* or *uspA2* gene. In these aspects nucleic acid probes of an appropriate length are prepared based on a consideration of the coding sequence of the *uspA1* or *uspA2* gene, or flanking regions near the *uspA1* or *uspA2* gene, such as regions downstream and upstream in the *M. catarrhalis* chromosome. The ability of such

nucleic acid probes to specifically hybridize to either *uspA1* or *uspA2* gene sequences lends them particular utility in a variety of embodiments. For example, the probes can be used in a variety of diagnostic assays for detecting the presence of pathogenic organisms in a given sample. In addition, these oligonucleotides can be inserted, in frame, into expression constructs for the purpose of screening the corresponding peptides for reactivity with existing antibodies or for the ability to generate diagnostic or therapeutic reagents.

To provide certain of the advantages in accordance with the invention, the preferred nucleic acid sequence employed for hybridization studies or assays includes sequences that are complementary to at least a 10 to 20, or so, nucleotide stretch of the sequence, although sequences of 30 to 60 or so nucleotides are also envisioned to be useful. A size of at least 9 nucleotides in length helps to ensure that the fragment will be of sufficient length to form a duplex molecule that is both stable and selective. Though molecules having complementary sequences over stretches greater than 10 bases in length are generally preferred, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of the specific hybrid molecules obtained. Thus, one will generally prefer to design nucleic acid molecules having either *uspA1* or *uspA2* gene-complementary stretches of 15 to 20 nucleotides, or even longer, such as 30 to 60, where desired. Such fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, by application of nucleic acid reproduction technology, such as the PCR™ technology of U.S. Patent 4,603,102, or by introducing selected sequences into recombinant vectors for recombinant production.

The probes that would be useful may be derived from any portion of the sequences of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16. Therefore, probes are specifically contemplated that comprise nucleotides 1 to 9, or 2 to 10, or 3 to 11 and so forth up to a probe comprising the last 9 nucleotides of the nucleotide sequence of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16. Thus, each probe would comprise at least about 9 linear nucleotides of the nucleotide sequence of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16., designated by the formula "n to n + 8," where n is an integer from 1 to the number of nucleotides in the sequence. Longer probes that hybridize to the *uspA1* or *uspA2* gene under low, medium, medium-high and high stringency conditions are

also contemplated, including those that comprise the entire nucleotide sequence of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16. This hypothetical may be repeated for probes having lengths of about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100 and greater bases.

In that the UspA antigenic epitopes of the present invention are believed to be indicative of pathogenic *Moraxella* species as exemplified by strains O35E, O46E, TTA24 and TTA37, the probes of the present invention will find particular utility as the basis for diagnostic hybridization assays for detecting UspA1 or UspA2 DNA in clinical samples. Exemplary clinical samples that can be used in the diagnosis of infections are thus any samples which could possibly include *Moraxella* nucleic acid, including middle ear fluid, sputum, mucus, bronchoalveolar fluid, amniotic fluid or the like. A variety of hybridization techniques and systems are known which can be used in connection with the hybridization aspects of the invention, including diagnostic assays such as those described in Falkow *et al.*, U.S. Patent 4,358,535. Depending on the application envisioned, one will desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of the probe toward the target sequence. For applications requiring a high degree of selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, for example, one will select relatively low salt and/or high temperature conditions, such as provided by 0.02M-0.15M NaCl at temperatures of 50°C to 70°C. These conditions are particularly selective, and tolerate little, if any, mismatch between the probe and the template or target strand.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent hybridization conditions are called for in order to allow formation of the heteroduplex. In these circumstances, one would desire to employ conditions such as 0.15M-0.9M salt, at temperatures ranging from 20°C to 55°C. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and the method of choice will generally depend on the desired results.

In certain embodiments, one may desire to employ nucleic acid probes to isolate variants from clone banks containing mutated clones. In particular embodiments, mutant clone colonies growing on solid media which contain variants of the *UspA1* and/or *UspA2* sequence could be identified on duplicate filters using hybridization conditions and methods, such as those used in colony blot assays, to obtain hybridization only between probes containing sequence variants and nucleic acid sequence variants contained in specific colonies. In this manner, small hybridization probes containing short variant sequences of either the *uspA1* or *uspA2* gene may be utilized to identify those clones growing on solid media which contain sequence variants of the entire *uspA1* or *uspA2* gene. These clones can then be grown to obtain desired quantities of the variant *UspA1* or *UspA2* nucleic acid sequences or the corresponding *UspA* antigen.

In clinical diagnostic embodiments, nucleic acid sequences of the present invention are used in combination with an appropriate means, such as a label, for determining hybridization. A wide variety of appropriate indicator means are known in the art, including radioactive, enzymatic or other ligands, such as avidin/biotin, which are capable of giving a detectable signal. In preferred diagnostic embodiments, one will likely desire to employ an enzyme tag such as urease, alkaline phosphatase or peroxidase, instead of radioactive or other environmental undesirable reagents. In the case of enzyme tags, colorimetric indicator substrates are known which can be employed to provide a means visible to the human eye or spectrophotometrically, to identify specific hybridization with pathogen nucleic acid-containing samples.

In general, it is envisioned that the hybridization probes described herein will be useful both as reagents in solution hybridizations as well as in embodiments employing a solid phase. In embodiments involving a solid phase, the test DNA (or RNA) from suspected clinical samples, such as exudates, body fluids (e.g., amniotic fluid, middle ear effusion, bronchoalveolar lavage fluid) or even tissues, is adsorbed or otherwise affixed to a selected matrix or surface. This fixed, single-stranded nucleic acid is then subjected to specific hybridization with selected probes under desired conditions. The selected conditions will depend on the particular circumstances based on the particular criteria required (depending, for example, on the G+C contents, type of target nucleic acid, source of nucleic acid, size of hybridization probe, etc.). Following washing of the hybridized surface so as to remove

nonspecifically bound probe molecules, specific hybridization is detected, or even quantified, by means of the label.

The nucleic acid sequences which encode for the UspA1 and/or UspA2 epitopes, or their variants, may be useful in conjunction with PCR™ methodology to detect *M. catarrhalis*. In general, by applying the PCR™ technology as set out, *e.g.*, in U.S. Patent 4,603,102, one may utilize various portions of either the *uspA1* or *uspA2* sequence as oligonucleotide probes for the PCR™ amplification of a defined portion of a *uspA1* or *uspA2* nucleic acid in a sample. The amplified portion of the *uspA1* or *uspA2* sequence may then be detected by hybridization with a hybridization probe containing a complementary sequence. In this manner, extremely small concentrations of *M. catarrhalis* nucleic acid may be detected in a sample utilizing *uspA1* or *uspA2* sequences.

3.0 Vectors, Host Cells and Cultures for Producing UspA1 and/or UspA2 Antigens

In order to express a UspA1 and/or UspA2 polypeptide, it is necessary to provide an *uspA1* and/or *uspA2* gene in an expression cassette. The expression cassette contains a UspA1 and/or UspA2-encoding nucleic acid under transcriptional control of a promoter. A "promoter" refers to a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a gene. The phrase "under transcriptional control" means that the promoter is in the correct location and orientation in relation to the nucleic acid to control RNA polymerase initiation and expression of the gene. Those promoters most commonly used in prokaryotic recombinant DNA construction include the B-lactamase (penicillinase) and lactose promoter systems (Chang *et al.*, 1978; Itakura *et al.*, 1977; Goeddel *et al.*, 1979) and a tryptophan (*trp*) promoter system (Goeddel *et al.*, 1980; EPO Appl. Publ. No. 0036776). While these are the most commonly used, other microbial promoters have been discovered and utilized, and details concerning their nucleotide sequences have been published, enabling a skilled worker to ligate them functionally with plasmid vectors (EPO Appl. Publ. No. 0036776). Additional examples of useful promoters are provided in Table IV below.

TABLE IV

Promoters	References
Immunoglobulin Heavy Chain	Hanerji <i>et al.</i> , 1983; Gilles <i>et al.</i> , 1983; Grosschedl and Baltimore, 1985; Atchinson and Perry, 1986, 1987; Imler <i>et al.</i> , 1987; Weinberger <i>et al.</i> , 1988; Kiledjian <i>et al.</i> , 1988; Porton <i>et al.</i> , 1990
Immunoglobulin Light Chain	Queen and Baltimore, 1983; Picard and Schaffner, 1984
T-Cell Receptor	Luria <i>et al.</i> , 1987, Winoto and Baltimore, 1989; Redondo <i>et al.</i> , 1990
HLA DQ α and DQ β	Sullivan and Peterlin, 1987
β -Interferon	Goodbourn <i>et al.</i> , 1986; Fujita <i>et al.</i> , 1987; Goodbourn and Maniatis, 1985
Interleukin-2	Greene <i>et al.</i> , 1989
Interleukin-2 Receptor	Greene <i>et al.</i> , 1989; Lin <i>et al.</i> , 1990
MHC Class II 5	Koch <i>et al.</i> , 1989
MHC Class II HLA-DRa	Sherman <i>et al.</i> , 1989
β -Actin	Kawamoto <i>et al.</i> , 1988; Ng <i>et al.</i> , 1989
Muscle Creatine Kinase	Jaynes <i>et al.</i> , 1988; Horlick and Benfield, 1989; Johnson <i>et al.</i> , 1989a
Prealbumin (Transthyretin)	Costa <i>et al.</i> , 1988
Elastase I	Omitz <i>et al.</i> , 1987
Metallothionein	Karin <i>et al.</i> , 1987; Culotta and Hamer, 1989
Collagenase	Pinkert <i>et al.</i> , 1987; Angel <i>et al.</i> , 1987
Albumin Gene	Pinkert <i>et al.</i> , 1987, Tronche <i>et al.</i> , 1989, 1990

TABLE IV (Continued)

Promoters	References
a-Fetoprotein	Godbout <i>et al.</i> , 1988; Campere and Tilghman, 1989
t-Globin	Bodine and Ley, 1987; Perez-Stable and Constantini, 1990
β -Globin	Trudel and Constantini, 1987
e-fos	Cohen <i>et al.</i> , 1987
c-HA-ras	Triesman, 1986; Deschamps <i>et al.</i> , 1985
Insulin	Edlund <i>et al.</i> , 1985
Neural Cell Adhesion Molecule (NCAM)	Hirsch <i>et al.</i> , 1990
α_1 -Antitrypsin	Latimer <i>et al.</i> , 1990
H2B (TH2B) Histone	Hwang <i>et al.</i> , 1990
Mouse or Type I Collagen	Ripe <i>et al.</i> , 1989
Glucose-Regulated Proteins (GRP94 and GRP78)	Chang <i>et al.</i> , 1989
Rat Growth Hormone	Larsen <i>et al.</i> , 1986
Human Serum Amyloid A (SAA)	Edbrooke <i>et al.</i> , 1989
Troponin I (TN I)	Yutzey <i>et al.</i> , 1989
Platelet-Derived Growth Factor	Pech <i>et al.</i> , 1989
Duchenne Muscular Dystrophy	Klamut <i>et al.</i> , 1990
SV40	Banerji <i>et al.</i> , 1981; Moreau <i>et al.</i> , 1981; Sleight and Lockett, 1985; Firak and Subramanian, 1986; Herr and Clarke, 1986; Imbra and Karin, 1986; Kadesch and Berg, 1986; Wang and Calame, 1986; Ondek <i>et al.</i> , 1987; Kuhl <i>et al.</i> , 1987; Schaffner <i>et al.</i> , 1988

TABLE IV (Continued)

Promoters	References
Polyoma	Swartzendruber and Lehman, 1975; Vasseur <i>et al.</i> , 1980; Katinka <i>et al.</i> , 1980, 1981; Tyndell <i>et al.</i> , 1981; Dandolo <i>et al.</i> , 1983; deVilliers <i>et al.</i> , 1984; Hen <i>et al.</i> , 1986; Satake <i>et al.</i> , 1988; Campbell and Villarreal, 1988
Retroviruses	Kriegler and Botchan, 1982, 1983; Levinson <i>et al.</i> , 1982; Kriegler <i>et al.</i> , 1983, 1984a,b, 1988; Bosze <i>et al.</i> , 1986; Miksicek <i>et al.</i> , 1986; Celander and Haseltine, 1987; Thiesen <i>et al.</i> , 1988; Celander <i>et al.</i> , 1988; Chol <i>et al.</i> , 1988; Reisman and Rotter, 1989
Papilloma Virus	Campo <i>et al.</i> , 1983; Lusky <i>et al.</i> , 1983; Spandidos and Wilkie, 1983; Spalholz <i>et al.</i> , 1985; Lusky and Botchan, 1986; Cripe <i>et al.</i> , 1987; Gloss <i>et al.</i> , 1987; Hirochika <i>et al.</i> , 1987, Stephens and Hentschel, 1987; Glue <i>et al.</i> , 1988
Hepatitis B Virus	Bulla and Siddiqui, 1986; Jameel and Siddiqui, 1986; Shaul and Ben-Levy, 1987; Spandau and Lee, 1988; Vannice and Levinson, 1988
Human Immunodeficiency Virus	Muesing <i>et al.</i> , 1987; Hauber and Cullan, 1988; Jakobovits <i>et al.</i> , 1988; Feng and Holland, 1988; Takebe <i>et al.</i> , 1988; Rowen <i>et al.</i> , 1988; Berkhout <i>et al.</i> , 1989; Laspia <i>et al.</i> , 1989; Sharp and Marciniak, 1989; Braddock <i>et al.</i> , 1989
Cytomegalovirus	Weber <i>et al.</i> , 1984; Boshart <i>et al.</i> , 1985; Foecking and Hofstetter, 1986
Gibbon Ape Leukemia Virus	Holbrook <i>et al.</i> , 1987; Quinn <i>et al.</i> , 1989

The appropriate expression cassette can be inserted into a commercially available expression vector by standard subcloning techniques. For example, the *E. coli* vectors pUC or pBluescript™ may be used according to the present invention to produce recombinant UspA1 and/or UspA2 polypeptide *in vitro*. The manipulation of these vectors is well known in the art. In general, plasmid vectors containing replicon and control sequences which are derived from species compatible with the host cell are used in connection with these hosts. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically transformed using pBR322, a plasmid derived from an *E. coli* species (Bolivar *et al.*, 1977). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR plasmid, or other microbial plasmid or phage must also contain, or be modified to contain, promoters which can be used by the microbial organism, for expression of its own proteins.

In addition, phage vectors containing replicon and control sequences that are compatible with the host microorganism can be used as a transforming vector in connection with these hosts. For example, the phage lambda GEM™-11 may be utilized in making recombinant phage vector which can be used to transform host cells, such as *E. coli* LE392.

In one embodiment, the UspA antigen is expressed as a fusion protein by using the pGEX4T-2 protein fusion system (Pharmacia LKB, Piscataway, NJ), allowing characterization of the UspA antigen as comprising both the UspA1 and UspA2 proteins. Additional examples of fusion protein expression systems are the glutathione S-transferase system (Pharmacia, Piscataway, NJ), the maltose binding protein system (NEB, Beverly, MA), the FLAG system (IBI, New Haven, CT), and the 6xHis system (Qiagen, Chatsworth, CA). Some of these fusion systems produce recombinant protein bearing only a small number of additional amino acids, which are unlikely to affect the functional capacity of the recombinant protein. For example, both the FLAG system and the 6xHis system add only short sequences, both of which are known to be poorly antigenic and which do not adversely affect folding of the protein to its native conformation. Other fusion systems produce proteins where it is desirable to excise the fusion partner from the desired protein. In another embodiment, the fusion partner is linked to the

recombinant protein by a peptide sequence containing a specific recognition sequence for a protease. Examples of suitable sequences are those recognized by the Tobacco Etch Virus protease (Life Technologies, Gaithersburg, MD) or Factor Xa (New England Biolabs, Beverly, MA).

5 *E. coli* is a preferred prokaryotic host. For example, *E. coli* strain RR1 is particularly useful. Other microbial strains which may be used include *E. coli* strains such as *E. coli* LE392, *E. coli* B, and *E. coli* X 1776 (ATCC No. 31537). The aforementioned strains, as well as *E. coli* W3110 (F-, lambda-, prototrophic, ATCC No. 273325), bacilli such as *Bacillus subtilis*, or other enterobacteriaceae such as *Salmonella typhimurium* or *Serratia marcescens*, and various
10 *Pseudomonas* species may be used. These examples are, of course, intended to be illustrative rather than limiting. Recombinant bacterial cells, for example *E. coli*, are grown in any of a number of suitable media, for example LB, and the expression of the recombinant polypeptide induced by adding IPTG to the media or switching incubation to a higher temperature. After culturing the bacteria for a further period of between 2 and 24 hours, the cells are collected by
15 centrifugation and washed to remove residual media. The bacterial cells are then lysed, for example, by disruption in a cell homogenizer and centrifuged to separate the dense inclusion bodies and cell membranes from the soluble cell components. This centrifugation can be performed under conditions whereby the dense inclusion bodies are selectively enriched by incorporation of sugars such as sucrose into the buffer and centrifugation at a selective speed.

20 If the recombinant protein is expressed in the inclusion bodies, as is the case in many instances, these can be washed in any of several solutions to remove some of the contaminating host proteins, then solubilized in solutions containing high concentrations of urea (e.g. 8M) or chaotropic agents such as guanidine hydrochloride in the presence of reducing agents such as β -mercaptoethanol or DTT (dithiothreitol).

25 Under some circumstances, it may be advantageous to incubate the polypeptide for several hours under conditions suitable for the protein to undergo a refolding process into a conformation which more closely resembles that of the native protein. Such conditions generally include low protein concentrations less than 500 μ g/ml, low levels of reducing agent, concentrations of urea

less than 2 M and often the presence of reagents such as a mixture of reduced and oxidized glutathione which facilitate the interchange of disulfide bonds within the protein molecule.

The refolding process can be monitored, for example, by SDS-PAGE or with antibodies which are specific for the native molecule (which can be obtained from animals vaccinated with the native molecule isolated from bacteria). Following refolding, the protein can then be purified further and separated from the refolding mixture by chromatography on any of several supports including ion exchange resins, gel permeation resins or on a variety of affinity columns.

There are a variety of other eukaryotic vectors that provide a suitable vehicle in which recombinant UspA proteins can be produced. In various embodiments of the invention, the expression construct may comprise a virus or engineered construct derived from a viral genome. The ability of certain viruses to enter cells via receptor-mediated endocytosis and to integrate into host cell genome and express viral genes stably and efficiently have made them attractive candidates for the transfer of foreign genes into mammalian cells (Ridgeway, 1988; Nicolas and Rubenstein, 1988; Baichwal and Sugden, 1986; Temin, 1986). The first viruses used as vectors were DNA viruses including the papovaviruses (simian virus 40 (SV40), bovine papilloma virus, and polyoma) (Ridgeway, 1988; Baichwal and Sugden, 1986) and adenoviruses (Ridgeway, 1988; Baichwal and Sugden, 1986) and adeno-associated viruses. Retroviruses also are attractive gene transfer vehicles (Nicolas and Rubenstein, 1988; Temin, 1986) as are vaccinia virus (Ridgeway, 1988) adeno-associated virus (Ridgeway, 1988) and herpes simplex virus (HSV) (Glorioso *et al.*, 1995). Such vectors may be used to (i) transform cell lines *in vitro* for the purpose of expressing proteins of interest or (ii) to transform cells *in vitro* or *in vivo* to provide therapeutic polypeptides in a gene therapy scenario.

With respect to eukaryotic vectors, the term promoter will be used here to refer to a group of transcriptional control modules that are clustered around the initiation site for RNA polymerase II. Much of the thinking about how promoters are organized derives from analyses of several viral promoters, including those for the HSV thymidine kinase (tk) and SV40 early transcription units. These studies, augmented by more recent work, have shown that promoters are composed of discrete functional modules, each consisting of approximately 7-20 bp of DNA, and containing one or more recognition sites for transcriptional activator or repressor proteins.

At least one module in each promoter functions to position the start site for RNA synthesis. The best known example of this is the TATA box, but in some promoters lacking a TATA box, such as the promoter for the mammalian terminal deoxynucleotidyl transferase gene and the promoter for the SV40 late genes, a discrete element overlying the start site itself helps to fix the place of initiation.

Additional promoter elements regulate the frequency of transcriptional initiation. Typically, these are located in the region 30-110 bp upstream of the start site, although a number of promoters have recently been shown to contain functional elements downstream of the start site as well. The spacing between promoter elements frequently is flexible, so that promoter function is preserved when elements are inverted or moved relative to one another. In the tk promoter, the spacing between promoter elements can be increased to 50 bp apart before activity begins to decline. Depending on the promoter, it appears that individual elements can function either cooperatively or independently to activate transcription.

The particular promoter that is employed to control the expression of a nucleic acid is not believed to be critical, so long as it is capable of expressing the nucleic acid in the targeted cell. Thus, where a human cell is targeted, it is preferable to position the nucleic acid coding region adjacent to and under the control of a promoter that is capable of being expressed in a human cell. Generally speaking, such a promoter might include either a human or viral promoter. Preferred promoters include those derived from HSV, including the $\alpha 4$ promoter. Another preferred embodiment is the tetracycline controlled promoter.

In various other embodiments, the human cytomegalovirus (CMV) immediate early gene promoter, the SV40 early promoter and the Rous sarcoma virus long terminal repeat can be used to obtain high-level expression of transgenes. The use of other viral or mammalian cellular or bacterial phage promoters which are well-known in the art to achieve expression of a transgene is contemplated as well, provided that the levels of expression are sufficient for a given purpose. Table IV lists several promoters which may be employed, in the context of the present invention, to regulate the expression of a transgene. This list is not intended to be exhaustive of all the possible elements involved in the promotion of transgene expression but, merely, to be exemplary thereof.

Enhancers were originally detected as genetic elements that increased transcription from a promoter located at a distant position on the same molecule of DNA. This ability to act over a large distance had little precedent in classic studies of prokaryotic transcriptional regulation. Subsequent work showed that regions of DNA with enhancer activity are organized much like promoters. That is, they are composed of many individual elements, each of which binds to one or more transcriptional proteins.

The basic distinction between enhancers and promoters is operational. An enhancer region as a whole must be able to stimulate transcription at a distance; this need not be true of a promoter region or its component elements. On the other hand, a promoter must have one or more elements that direct initiation of RNA synthesis at a particular site and in a particular orientation, whereas enhancers lack these specificities. Promoters and enhancers are often overlapping and contiguous, often seeming to have a very similar modular organization. Table V lists several enhancers, of course, this list is not meant to be limiting but exemplary.

TABLE V

Enhancer	Inducer	References
MT II	Phorbol Ester (TFA) Heavy metals	Palmiter <i>et al.</i> , 1982; Haslinger and Karin, 1985; Searle <i>et al.</i> , 1985; Stuart <i>et al.</i> , 1985; Imagawa <i>et al.</i> , 1987; Karin ®, 1987; Angel <i>et al.</i> , 1987b; McNeall <i>et al.</i> , 1989
MMTV (mouse mammary tumor virus)	Glucocorticoids	Huang <i>et al.</i> , 1981; Lee <i>et al.</i> , 1981; Majors and Varmus, 1983; Chandler <i>et al.</i> , 1983; Lee <i>et al.</i> , 1984; Fonta <i>et al.</i> , 1985; Sakai <i>et al.</i> , 1986
β-Interferon	poly(rl)X poly(rc)	Tavernier <i>et al.</i> , 1983
Adenovirus 5 E2	Ela	Imperiale and Nevins, 1984
Collagenase	Phorbol Ester (TPA)	Angle <i>et al.</i> , 1987a
Stromelysin	Phorbol Ester (TPA)	Angle <i>et al.</i> , 1987b

TABLE V (Continued)

Enhancer	Inducer	References
SV40	Phorbol Ester (TFA)	Angel <i>et al.</i> , 1987b
Murine MX Gene	Interferon, Newcastle Disease Virus	
GRP78 Gene	A23187	Resendez <i>et al.</i> , 1988
a-2-Macroglobulin	IL-6	Kunz <i>et al.</i> , 1989
Vimentin	Serum	Rittling <i>et al.</i> , 1989
MHC Class I Gene H-2kb	Interferon	Blonar <i>et al.</i> , 1989
HSP70	Ela, SV40 Large T Antigen	Taylor <i>et al.</i> , 1989; Taylor and Kingston, 1990a,b
Proliferin	Phorbol Ester-TPA	Mordacq and Linzer, 1989
Tumor Necrosis Factor	FMA	Hensel <i>et al.</i> , 1989
Thyroid Stimulating Hormone a Gene	Thyroid Hormone	Chatterjee <i>et al.</i> , 1989

Additionally any promoter/enhancer combination (as per the Eukaryotic Promoter Data Base EPDB) could also be used to drive expression of a transgene. Use of a T3, T7 or SP6 cytoplasmic expression system is another possible embodiment. Eukaryotic cells can support cytoplasmic transcription from certain bacterial promoters if the appropriate bacterial polymerase is provided, either as part of the delivery complex or as an additional genetic expression construct.

Host cells include eukaryotic microbes, such as yeast cultures may also be used. *Saccharomyces cerevisiae*, or common baker's yeast is the most commonly used among eukaryotic microorganisms, although a number of other strains are commonly available. For expression in *Saccharomyces*, the plasmid YRp7, for example, is commonly used (Stinchcomb *et al.*, 1979; Kingsman *et al.*, 1979; Tschemper *et al.*, 1980). This plasmid already contains the

trp1 gene which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan. for example ATCC No. 44076 or PEP4-1 (Jones, 1977). The presence of the *trp1* lesion as a characteristic of the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan.

5 Suitable promoting sequences in yeast vectors include the promoters for 3-phosphoglycerate kinase (Hitzeman *et al.*, 1980) or other glycolytic enzymes (Hess *et al.*, 1968; Holland *et al.*, 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose
10 isomerase, and glucokinase. In constructing suitable expression plasmids, the termination sequences associated with these genes are also ligated into the expression vector 3' of the sequence desired to be expressed to provide polyadenylation of the mRNA and termination. Other promoters, which have the additional advantage of transcription controlled by growth conditions are the promoter region for alcohol dehydrogenase 2, isocytochrome C, acid
15 phosphatase, degradative enzymes associated with nitrogen metabolism, and the aforementioned glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Any plasmid vector containing a yeast-compatible promoter, origin of replication and termination sequences is suitable.

In addition to eukaryotic microorganisms, cultures of cells derived from multicellular organisms
20 may also be used as hosts. In principle, any such cell culture is workable, whether from vertebrate or invertebrate culture. However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure in recent years (*Tissue Culture*, 1973). Examples of such useful host cell lines are VERO and HeLa cells, Chinese hamster ovary (CHO) cell lines, and W138, BHK, COS-7, 293 and MDCK
25 cell lines. Expression vectors for such cells ordinarily include (if necessary) an origin of replication, a promoter located in front of the gene to be expressed, along with any necessary ribosome binding sites, RNA splice sites, polyadenylation site, and transcriptional terminator sequences.

4.0 Preparation of Antibodies to UspA Proteins

Antibodies to UspA1 or UspA2 peptides or polypeptides may be readily prepared through use of well-known techniques, such as those exemplified in U.S. Patent 4,196,265. Typically, this technique involves immunizing a suitable animal with a selected immunogen composition, *e.g.*, purified or partially purified protein, synthetic protein or fragments thereof, as discussed in the section on vaccines. Animals to be immunized are mammals such as cats, dogs and horses, although there is no limitation other than that the subject be capable of mounting an immune response of some kind. The immunizing composition is administered in a manner effective to stimulate antibody producing cells. Rodents such as mice and rats are preferred animals, however, the use of rabbit, sheep or frog cells is possible. The use of rats may provide certain advantages, but mice are preferred, with the BALB/c mouse being most preferred as the most routinely used animal and one that generally gives a higher percentage of stable fusions.

For generation of monoclonal antibodies (MAbs), following immunization, somatic cells with the potential for producing antibodies, specifically B lymphocytes (B cells), are selected for use in the MAb generating protocol. These cells may be obtained from biopsied spleens, tonsils or lymph nodes, or from a peripheral blood sample. Spleen cells and peripheral blood cells are preferred, the former because they are a rich source of antibody-producing cells that are in the dividing plasmablast stage, and the latter because peripheral blood is easily accessible. Often, a panel of animals will have been immunized and the spleen of the animal with the highest antibody titer removed. Spleen lymphocytes are obtained by homogenizing the spleen with a syringe. Typically, a spleen from an immunized mouse contains approximately 5×10^7 to 2×10^8 lymphocytes.

The antibody-producing B cells from the immunized animal are then fused with cells of an immortal myeloma cell line, generally one of the same species as the animal that was immunized. Myeloma cell lines suited for use in hybridoma-producing fusion procedures preferably are non-antibody-producing, have high fusion efficiency and enzyme deficiencies that render them incapable of growing in certain selective media which support the growth of only the desired fused cells, called "hybridomas."

Any one of a number of myeloma cells may be used and these are known to those of skill in the art. For example, where the immunized animal is a mouse, one may use P3-X63/Ag8, X63-Ag8.653, NS1/1.Ag 4 1, Sp210-Ag14, FO, NSO/U, MPC-11, MPC11-X45-GTG 1.7 and S194/5XX0 Bul; for rats, one may use R210.RCY3, Y3-Ag 1.2.3, IR983F and 4B210; and U-266, GM1500-GRG2, LICR-LON-HMy2 and UC729-6 are all useful in connection with human cell fusions.

One preferred murine myeloma cell line is the NS-1 myeloma cell line (also termed P3-NS-1-Ag4-1), which is readily available from the NIGMS Human Genetic Mutant Cell Repository by requesting cell line repository number GM3573. Another mouse myeloma cell line that may be used is the 8-azaguanine-resistant mouse murine myeloma SP2/0 non-producer cell line.

Methods for generating hybrids of antibody-producing spleen or lymph node cells and myeloma cells usually comprise mixing somatic cells with myeloma cells in a 2:1 proportion, though the proportion may vary from about 20:1 to about 1:1, respectively, in the presence of an agent or agents (chemical or electrical) that promote the fusion of cell membranes. Fusion methods using Sendai virus have been described by Kohler & Milstein (1975; 1976), and those using polyethylene glycol (PEG), such as 37% (v/v) PEG, by Gefter *et al.* (1977). The use of electrically induced fusion methods is also appropriate.

Fusion procedures usually produce viable hybrids at low frequencies, about 1×10^{-6} to 1×10^{-8} . This does not pose a problem, however, as the viable, fused hybrids are differentiated from the parental, unfused cells (particularly the unfused myeloma cells that would normally continue to divide indefinitely) by culture in a selective medium. The selective medium generally is one that contains an agent that blocks the *de novo* synthesis of nucleotides in the tissue culture media. Exemplary and preferred agents are aminopterin, methotrexate and azaserine. Aminopterin and methotrexate block *de novo* synthesis of both purines and pyrimidines, whereas azaserine blocks only purine synthesis. Where aminopterin or methotrexate is used, the media is supplemented with hypoxanthine and thymidine as a source of nucleotides (HAT medium). Where azaserine is used, the media is supplemented with hypoxanthine.

The preferred selection medium is HAT. Only cells capable of operating nucleotide salvage pathways are able to survive in HAT medium. The myeloma cells are defective in key enzymes of the salvage pathway, *e.g.*, hypoxanthine phosphoribosyl transferase (HPRT), and they cannot survive. The B cells can operate this pathway, but they have a limited life span in culture and generally die within about two weeks. Therefore, the only cells that can survive in the selective media are those hybrids formed from myeloma and B cells.

This culturing provides a population of hybridomas from which specific hybridomas are selected. Typically, selection of hybridomas is performed by single-clone dilution in microtiter plates, followed by testing the individual clonal supernatants (after about two to three weeks) for the desired reactivity. The assay should be sensitive, simple and rapid, such as radioimmunoassays, enzyme immunoassays, cytotoxicity assays, plaque assays, dot immunobinding assays, and the like.

The selected hybridomas are then serially diluted and cloned into individual antibody-producing cell lines, which clones can then be propagated indefinitely to provide MAbs. The cell lines may be exploited for MAb production in two basic ways. A sample of the hybridoma can be injected, usually in the peritoneal cavity, into a histocompatible animal of the type that was used to provide the somatic and myeloma cells for the original fusion. The injected animal develops tumors secreting the specific monoclonal antibody produced by the fused cell hybrid. The body fluids of the animal, such as serum or ascites fluid, can then be tapped to provide MAbs in high concentration. The individual cell lines could also be cultured *in vitro*, where the MAbs are naturally secreted into the culture medium from which they can be readily obtained in high concentrations. MAbs produced by either means may be further purified, if desired, using filtration, centrifugation and various chromatographic methods such as HPLC or affinity chromatography.

Monoclonal antibodies of the present invention also include anti-idiotypic antibodies produced by methods well-known in the art. Monoclonal antibodies according to the present invention also may be monoclonal heteroconjugates, *i.e.*, hybrids of two or more antibody molecules. In another embodiment, monoclonal antibodies according to the invention are chimeric monoclonal antibodies. In one approach, the chimeric monoclonal antibody is engineered by cloning recombinant DNA containing the promoter, leader, and variable-region

sequences from a mouse antibody producing cell and the constant-region exons from a human antibody gene. The antibody encoded by such a recombinant gene is a mouse-human chimera. Its antibody specificity is determined by the variable region derived from mouse sequences. Its isotype, which is determined by the constant region, is derived from human DNA.

5 In another embodiment, the monoclonal antibody according to the present invention is a "humanized" monoclonal antibody, produced by techniques well-known in the art. That is, mouse complementary determining regions ("CDRs") are transferred from heavy and light V-chains of the mouse Ig into a human V-domain, followed by the replacement of some human residues in the framework regions of their murine counterparts. "Humanized" monoclonal
10 antibodies in accordance with this invention are especially suitable for use in *in vivo* diagnostic and therapeutic methods for treating *Moraxella* infections.

As stated above, the monoclonal antibodies and fragments thereof according to this invention can be multiplied according to *in vitro* and *in vivo* methods well-known in the art. Multiplication *in vitro* is carried out in suitable culture media such as Dulbecco's modified
15 Eagle medium or RPMI 1640 medium, optionally replenished by a mammalian serum such as fetal calf serum or trace elements and growth-sustaining supplements, *e.g.*, feeder cells, such as normal mouse peritoneal exudate cells, spleen cells, bone marrow macrophages or the like. *In vitro* production provides relatively pure antibody preparations and allows scale-up to give large amounts of the desired antibodies. Techniques for large scale hybridoma cultivation under
20 tissue culture conditions are known in the art and include homogenous suspension culture, *e.g.*, in an airlift reactor or in a continuous stirrer reactor or immobilized or entrapped cell culture.

Large amounts of the monoclonal antibody of the present invention also may be obtained by multiplying hybridoma cells *in vivo*. Cell clones are injected into mammals which are histocompatible with the parent cells, *e.g.*, syngeneic mice, to cause growth of
25 antibody-producing tumors. Optionally, the animals are primed with a hydrocarbon, especially oils such as Pristane (tetramethylpentadecane) prior to injection.

In accordance with the present invention, fragments of the monoclonal antibody of the invention can be obtained from monoclonal antibodies produced as described above, by methods which include digestion with enzymes such as pepsin or papain and/or cleavage of

disulfide bonds by chemical reduction. Alternatively, monoclonal antibody fragments encompassed by the present invention can be synthesized using an automated peptide synthesizer, or they may be produced manually using techniques well known in the art.

The monoclonal conjugates of the present invention are prepared by methods known in the art, *e.g.*, by reacting a monoclonal antibody prepared as described above with, for instance, an enzyme in the presence of a coupling agent such as glutaraldehyde or periodate. Conjugates with fluorescein markers are prepared in the presence of these coupling agents, or by reaction with an isothiocyanate. Conjugates with metal chelates are similarly produced. Other moieties to which antibodies may be conjugated include radionuclides such as ^3H , ^{125}I , ^{131}I , ^{32}P , ^{35}S , ^{14}C , ^{51}Cr , ^{36}Cl , ^{57}Co , ^{58}Co , ^{59}Fe , ^{75}Se , ^{152}Eu , and $^{99\text{m}}\text{Tc}$, are other useful labels which can be conjugated to antibodies. Radio-labeled monoclonal antibodies of the present invention are produced according to well-known methods in the art. For instance, monoclonal antibodies can be iodinated by contact with sodium or potassium iodide and a chemical oxidizing agent such as sodium hypochlorite, or an enzymatic oxidizing agent, such as lactoperoxidase. Monoclonal antibodies according to the invention may be labeled with technetium- $^{99\text{m}}$ by ligand exchange process, for example, by reducing pertechnetate with stannous solution, chelating the reduced technetium onto a Sephadex column and applying the antibody to this column or by direct labeling techniques, *e.g.*, by incubating pertechnetate, a reducing agent such as SNCl_2 , a buffer solution such as sodium-potassium phthalate solution, and the antibody.

5.0 Use of Peptides and Monoclonal Antibodies in Immunoassays

It is proposed that the monoclonal antibodies of the present invention will find useful application in standard immunochemical procedures, such as ELISA and western blot methods, as well as other procedures which may utilize antibodies specific to CopB epitopes. While ELISAs are preferred, it will be readily appreciated that such assays include RIAs and other non-enzyme linked antibody binding assays or procedures. Additionally, it is proposed that monoclonal antibodies specific to the particular UspA epitope may be utilized in other useful applications. For example, their use in immunoabsorbent protocols may be useful in purifying native or recombinant UspA proteins or variants thereof.

It also is proposed that the disclosed UspA1 and UspA2 peptides of the invention will find use as antigens for raising antibodies and in immunoassays for the detection of anti-UspA

antigen-reactive antibodies. In a variation on this embodiment, UspA1 and UspA2 mutant peptides may be screened, in immunoassay format, for reactivity against UspA1- or UspA2-specific antibodies, such as MAb 17C7. In this way, a mutational analysis of various epitopes may be performed. Results from such analyses may then be used to determine which additional UspA1 or UspA2 epitopes may be recognized by antibodies and useful in the preparation of potential vaccines for *Moraxella*.

Diagnostic immunoassays include direct culturing of bodily fluids, either in liquid culture or on a solid support such as nutrient agar. A typical assay involves collecting a sample of bodily fluid from a patient and placing the sample in conditions optimum for growth of the pathogen. The determination can then be made as to whether the microbe exists in the sample. Further analysis can be carried out to determine the hemolyzing properties of the microbe.

Immunoassays encompassed by the present invention include, but are not limited to those described in U.S. Patent No. 4,367,110 (double monoclonal antibody sandwich assay) and U.S. Patent No. 4,452,901 (western blot). Other assays include immunoprecipitation of labeled ligands and immunocytochemistry, both *in vitro* and *in vivo*.

Immunoassays, in their most simple and direct sense, are binding assays. Certain preferred immunoassays are the various types of enzyme linked immunosorbent assays (ELISAs) and radioimmunoassays (RIAs) known in the art. Immunohistochemical detection using tissue sections is also particularly useful. However, it will be readily appreciated that detection is not limited to such techniques, and western blotting, dot blotting, FACS analyses, and the like may also be used.

In one exemplary ELISA, the anti-UspA antibodies of the invention are immobilized onto a selected surface exhibiting protein affinity, such as a well in a polystyrene microtiter plate. Then, a test composition suspected of containing the desired antigen, such as a clinical sample, is added to the wells. After binding and washing to remove non-specifically bound immune complexes, the bound antigen may be detected. Detection is generally achieved by the addition of another antibody, specific for the desired antigen, that is linked to a detectable label. This type of ELISA is a simple "sandwich ELISA". Detection may also be achieved by the addition of a second antibody specific for the desired antigen, followed by the addition of a

third antibody that has binding affinity for the second antibody, with the third antibody being linked to a detectable label.

In another exemplary ELISA, the samples suspected of containing the UspA antigen are immobilized onto the well surface and then contacted with the anti-UspA antibodies. After binding and appropriate washing, the bound immune complexes are detected. Where the initial antigen specific antibodies are linked to a detectable label, the immune complexes may be detected directly. Again, the immune complexes may be detected using a second antibody that has binding affinity for the first antigen specific antibody, with the second antibody being linked to a detectable label.

Further methods include the detection of primary immune complexes by a two step approach. A second binding ligand, such as an antibody, that has binding affinity for the primary antibody is used to form secondary immune complexes, as described above. After washing, the secondary immune complexes are contacted with a third binding ligand or antibody that has binding affinity for the second antibody, again under conditions effective and for a period of time sufficient to allow the formation of immune complexes (tertiary immune complexes). The third ligand or antibody is linked to a detectable label, allowing detection of the tertiary immune complexes thus formed. This system may provide for signal amplification if desired.

Competition ELISAs are also possible in which test samples compete for binding with known amounts of labeled antigens or antibodies. The amount of reactive species in the unknown sample is determined by mixing the sample with the known labeled species before or during incubation with coated wells. (Antigen or antibodies may also be linked to a solid support, such as in the form of beads, dipstick, membrane or column matrix, and the sample to be analyzed applied to the immobilized antigen or antibody.) The presence of reactive species in the sample acts to reduce the amount of labeled species available for binding to the well and thus reduces the ultimate signal.

Irrespective of the format employed, ELISAs have certain features in common, such as coating, incubating or binding, washing to remove non-specifically bound species, and detecting the bound immune complexes. These are described below.

In coating a plate with either antigen or antibody, one will generally incubate the wells of the plate with a solution of the antigen or antibody, either overnight or for a specified period. The wells of the plate will then be washed to remove incompletely adsorbed material. Any remaining available surfaces of the wells are then "coated" with a nonspecific protein that is antigenically neutral with regard to the test antisera. These include bovine serum albumin (BSA), casein and solutions of milk powder. The coating allows for blocking of nonspecific adsorption sites on the immobilizing surface and thus reduces the background caused by nonspecific binding of antisera onto the surface.

After binding of antigenic material to the well, coating with a non-reactive material to reduce background, and washing to remove unbound material, the immobilizing surface is contacted with the antisera or clinical or biological extract to be tested in a manner conducive to immune complex (antigen/antibody) formation. Such conditions preferably include diluting the antisera with diluents such as BSA, bovine gamma globulin (BGG) and phosphate buffered saline (PBS)/Tween. These added agents also tend to assist in the reduction of nonspecific background. The layered antisera is then allowed to incubate for from 2 to 4 hours, at temperatures preferably on the order of 25° to 27°C. Following incubation, the antisera-contacted surface is washed so as to remove non-immunocomplexed material. A preferred washing procedure includes washing with a solution such as PBS/Tween, or borate buffer.

Following formation of specific immunocomplexes between the test sample and the bound antigen, and subsequent washing, the occurrence and even amount of immunocomplex formation may be determined by subjecting same to a second antibody having specificity for the first. Of course, in that the test sample will typically be of human origin, the second antibody will preferably be an antibody having specificity in general for human IgG. To provide a detecting means, the second antibody will preferably have an associated enzyme that will generate a color development upon incubating with an appropriate chromogenic substrate. Thus, for example, one will desire to contact and incubate the antisera-bound surface with a urease or peroxidase-conjugated anti-human IgG for a period of time and under conditions which favor the development of immunocomplex formation (*e.g.*, incubation for 2 hours at room temperature in a PBS-containing solution such as PBS-Tween).

After incubation with the second enzyme-tagged antibody, and subsequent to washing to remove unbound material, the amount of label is quantified by incubation with a chromogenic substrate such as urea and bromocresol purple or 2,2'-azino-di-(3-ethyl-benzthiazoline-6-sulfonic acid [ABTS] and H₂O₂, in the case of peroxidase as the enzyme label. Quantification is then achieved by measuring the degree of color generation. *e.g.*, using a visible spectra spectrophotometer. Alternatively, the label may be a chemilluminescent one. The use of such labels is described in U.S. Patent Nos. 5,310,687, 5,238,808 and 5,221,605.

6.0 Prophylactic Use of UspA Peptides and UspA-Specific Antibodies

In a further embodiment of the present invention, there are provided methods for active and passive immunoprophylaxis. Active immunoprophylaxis will be discussed first, followed by a discussion on passive immunoprophylaxis. It should be noted that the discussion of formulating vaccine compositions in the context of active immunotherapy is relevant to the raising antibodies in experimental animals for passive immunotherapy and for the generation of diagnostic methods.

6.1 Active Immunotherapy

According to the present invention, UspA1 or UspA2 polypeptides or UspA1- or UspA2-derived peptides, as discussed above, may be used as vaccine formulations to generate protective anti-*M. catarrhalis* antibody responses *in vivo*. By protective, it is only meant that the immune system of a treated individual is capable of generating a response that reduces, to any extent, the clinical impact of the bacterial infection. This may range from a minimal decrease in bacterial burden to outright prevention of infection. Ideally, the treated subject will not exhibit the more serious clinical manifestations of *M. catarrhalis* infection.

Generally, immunoprophylaxis involves the administration, to a subject at risk, of a vaccine composition. In the instant case, the vaccine composition will contain a UspA1 and/or UspA2 polypeptide or immunogenic derivative thereof in a pharmaceutically acceptable carrier, diluent or excipient. As stated above, those of skill in the art are able, through a variety of mechanisms, to identify appropriate antigenic characteristics of UspA1 and UspA2 and, in so doing, develop vaccines that will achieve generation of immune responses against *M. catarrhalis*.

The stability and immunogenicity of UspA1 and UspA2 antigens may vary and, therefore, it may be desirable to couple the antigen to a carrier molecule. Exemplary carriers are KLH, BSA, human serum albumin, myoglobin, β -galactosidase, penicillinase, CRM₁₉₇ and bacterial toxoids, such as diphtheria toxoid and tetanus toxoid. Those of skill in the art are aware of proper methods by which peptides can be linked to carriers without destroying their immunogenic value. Synthetic carriers such as multi-poly-DL-alanyl-poly-L-lysine and poly-L-lysine also are contemplated. Coupling generally is accomplished through amino or carboxyl-terminal residues of the antigen, thereby affording the peptide or polypeptide the greatest chance of assuming a relatively "native" conformation following coupling.

It is recognized that other protective agents could be coupled with either a UspA1 or UspA2 antigen such that the UspA1 or UspA2 antigen acts as the carrier molecule. For example, agents which protect against other pathogenic organisms, such as bacteria, viruses or parasites, could be coupled to either a UspA1 or UspA2 antigen to produce a multivalent vaccine or pharmaceutical composition which would be useful for the treatment or inhibition of both *M. catarrhalis* infection and other pathogenic infections. In particular, it is envisioned that either UspA1 or UspA2 proteins or peptides could serve as immunogenic carriers for other vaccine components, for example, saccharides of pneumococcus, meningococcus or hemophylus influenza and could even be covalently coupled to these other components.

It also may be desirable to include in the composition any of a number of different substances referred to as adjuvants, which are known to stimulate the appropriate portion of the immune system of the vaccinated animal. Suitable adjuvants for the vaccination of subjects (including experimental animals) include, but are not limited to oil emulsions such as Freund's complete or incomplete adjuvant (not suitable for livestock use), Marcol 52:Montanide 888 (Marcol is a Trademark of Esso, Montanide is a Trademark of SEPPIC, Paris), squalane or squalene, Adjuvant 65 (containing peanut oil, mannide monooleate and aluminum monostearate), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI ImmunoChem Research Inc., Hamilton, Utah), Stimulon™ (QS-21; Aquila Biopharmaceuticals Inc., Wooster, MA), mineral gels such as aluminum hydroxide, aluminum phosphate, calcium phosphate and alum, surfactants such as hexadecylamine, octadecylamine, lysolecithin, dimethyldioctadecylammonium bromide, N,N-dioctadecyl-N,N'-bis(2-hydroxyethyl)-propanediamine, methoxyhexadecylglycerol and pluronic polyols, polyanions such as pyran, dextran sulfate,

polyacrylic acid and carbopol, peptides and amino acids such as muramyl dipeptide, dimethylglycine, tuftsin and trehalose dimycolate. Agents include synthetic polymers of sugars (Carbopol), emulsion in physiologically acceptable oil vehicles such as mannide mono-oleate (Aracel A) or emulsion with 20 percent solution of a perfluorocarbon (Fluosol-DA) also may be employed.

The preparation of vaccines which contain peptide sequences as active ingredients is generally well understood in the art, as exemplified by U.S. Patents 4,608,251; 4,601,903; 4,599,231; 4,599,230; 4,596,792; and 4,578,770, all incorporated herein by reference. Typically, such vaccines are prepared as injectables. Either as liquid solutions or suspensions: Solid forms suitable for solution in, or suspension in, liquid prior to injection may also be prepared. The preparation may also be emulsified. The active immunogenic ingredient is often mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the vaccine may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, or adjuvants which enhance the effectiveness of the vaccines.

The vaccine preparations of the present invention also can be administered following incorporation into non-toxic carriers such as liposomes or other microcarrier substances, or after conjugation to polysaccharides, proteins or polymers or in combination with Quil-A to form "iscoms" (immunostimulating complexes). These complexes can serve to reduce the toxicity of the antigen, delay its clearance from the host and improve the immune response by acting as an adjuvant. Other suitable adjuvants for use this embodiment of the present invention include INF, IL-2, IL-4, IL-8, IL-12 and other immunostimulatory compounds. Further, conjugates comprising the immunogen together with an integral membrane protein of prokaryotic origin, such as TraT (see PCT/AU87/00107) may prove advantageous.

The vaccines are conventionally administered parenterally, by injection, for example, either subcutaneously or intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. For suppositories, traditional binders and carriers may include, for example, polyalkylene glycols or triglycerides: such suppositories may be formed from mixtures containing the active ingredient

in the range of 0.5% to 10%, preferably 1-2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate and the like. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain 10-95% of active ingredient, preferably 25-70%.

The peptides may be formulated into the vaccine as neutral or salt forms. Pharmaceutically acceptable salts, include the acid addition salts (formed with the free amino groups of the peptide) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups may also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

The vaccines are administered in a manner compatible with the dosage formulation, and in such amount as will be therapeutically effective and immunogenic. The quantity to be administered depends on the subject to be treated, including, *e.g.*, the capacity of the individual's immune system to synthesize antibodies, and the degree of protection desired. Precise amounts of active ingredient required to be administered depend on the judgment of the practitioner. However, suitable dosage ranges are of the order of several hundred micrograms active ingredient per vaccination. Suitable regimes for initial administration and booster shots are also variable, but are typified by an initial administration followed by subsequent inoculations or other administrations.

The manner of application may be varied widely. Any of the conventional methods for administration of a vaccine are applicable. These are believed to include oral application on a solid physiologically acceptable base or in a physiologically acceptable dispersion, parenterally, by injection or the like. The dosage of the vaccine will depend on the route of administration and will vary according to the size of the host.

In many instances, it will be desirable to have multiple administrations of the vaccine, usually not exceeding six vaccinations, more usually not exceeding four vaccinations and

preferably one or more, usually at least about three vaccinations. The vaccinations will normally be at from two to twelve week intervals, more usually from three to five week intervals. Periodic boosters at intervals of 1-5 years, usually three years, will be desirable to maintain protective levels of the antibodies. The course of the immunization may be followed by assays for antibodies for the supernatant antigens. The assays may be performed by labeling with conventional labels, such as radionuclides, enzymes, fluorescers, and the like. These techniques are well known and may be found in a wide variety of patents, such as U.S. Patent Nos. 3,791,932; 4,174,384 and 3,949,064, as illustrative of these types of assays.

6.2 Passive Immunotherapy

Passive immunity is defined, for the purposes of this application, as the transfer to an organism of an immune response effector that was generated in another organism. The classic example of establishing passive immunity is to transfer antibodies produced in one organism into a second, immunologically compatible animal. By "immunologically compatible," it is meant that the antibody can perform at least some of its immune functions in the new host animal. More recently, as a better understanding of cellular immune functions has evolved, it has become possible to accomplish passive immunity by transferring other effectors, such as certain kinds of lymphocytes, including cytotoxic and helper T cells, NK cells and other immune effector cells. The present invention contemplates both of these approaches.

Antibodies, antisera and immune effector cells are raised using standard vaccination regimes in appropriate animals, as discussed above. The primary animal is vaccinated with at least a microbe preparation or one bacterial product or by-product according to the present invention, with or without an adjuvant, to generate an immune response. The immune response may be monitored, for example, by measurement of the levels of antibodies produced, using standard ELISA methods.

Once an adequate immune response has been generated, immune effector cells can be collected on a regular basis, usually from blood draws. The antibody fraction can be purified from the blood by standard means, *e.g.*, by protein A or protein G chromatography. In an alternative preferred embodiment, monoclonal antibody-producing hybridomas are prepared by standard means (Coligan *et al.*, 1991). Monoclonal antibodies are then prepared from the hybridoma cells by standard means. If the primary host's monoclonal antibodies are not

compatible with the animal to be treated, it is possible that genetic engineering of the cells can be employed to modify the antibody to be tolerated by the animal to be treated. In the human context, murine antibodies, for example, may be "humanized" in this fashion.

Antibodies, antisera or immune effector cells, prepared as set forth above, are injected
5 into hosts to provide passive immunity against microbial infestation. For example, an antibody composition is prepared by mixing, preferably homogeneously mixing, at least one antibody with at least one pharmaceutically or veterinarily acceptable carrier, diluent, or excipient using standard methods of pharmaceutical or veterinary preparation. The amount of antibody
10 required to produce a single dosage form will vary depending upon the microbial species being vaccinated against, the individual to be treated and the particular mode of administration. The specific dose level for any particular individual will depend upon a variety of factors including the age, body weight, general health, sex, and diet of the individual, time of administration, route of administration, rate of excretion, drug combination and the severity of the microbial infestation.

15 The antibody composition may be administered intravenously, subcutaneously, intranasally, orally, intramuscularly, vaginally, rectally, topically or via any other desired route. Repeated dosings may be necessary and will vary, for example, depending on the clinical setting, the particular microbe, the condition of the patient and the use of other therapies.

6.3 DNA Immunization HC

20 The invention also relates to a vaccine comprising a nucleic acid molecule encoding a UspA1, UspA2 protein or a peptide comprising SEQ ID NO:17 wherein said UspA1, UspA2 protein or peptide retains immunogenicity and, when incorporated into an immunogenic composition or vaccine and administered to a vertebrate, provides protection without inducing enhanced disease upon subsequent infection of the vertebrate with *M. catarrhalis*, and a
25 physiologically acceptable vehicle. Such a vaccine is referred to herein as a nucleic acid vaccine or DNA vaccine and is useful for the genetic immunization of vertebrates.

The term, "genetic immunization", as used herein, refers to inoculation of a vertebrate, particularly a mammal such as a mouse or human, with a nucleic acid vaccine directed against a pathogenic agent, particularly *M. catarrhalis*, resulting in protection of the vertebrate against *M.*

5 *catarrhalis*. A "nucleic acid vaccine" or "DNA vaccine" as used herein, is a nucleic acid construct comprising a nucleic acid molecule encoding UspA1, UspA2 or an immunogenic epitope comprising SEQ ID NO:17. The nucleic acid construct can also include transcriptional promoter elements, enhancer elements, splicing signals, termination and polyadenylation signals, and other nucleic acid sequences.

10 The nucleic acid vaccine can be produced by standard methods. For example, using known methods, a nucleic acid (*e.g.*, DNA) encoding UspA1 or UspA2 can be inserted into an expression vector to construct a nucleic acid vaccine (see Maniatis *et al.*, 1989). The individual vertebrate is inoculated with the nucleic acid vaccine (*i.e.*, the nucleic acid vaccine is administered), using standard methods. The vertebrate can be inoculated subcutaneously, intravenously, intraperitoneally, intradermally, intramuscularly, topically, orally, rectally, nasally, buccally, vaginally, by inhalation spray, or via an implanted reservoir in dosage formulations containing conventional non-toxic, physiologically acceptable carriers or vehicles. Alternatively, the vertebrate is inoculated with the nucleic acid vaccine through the use of a particle acceleration instrument (a "gene gun"). The form in which it is administered (*e.g.*, capsule, tablet, solution, emulsion) will depend in part on the route by which it is administered. For example, for mucosal administration, nose drops, inhalants or suppositories can be used.

15 The nucleic acid vaccine can be administered in conjunction with any suitable adjuvant. The adjuvant is administered in a sufficient amount, which is that amount that is sufficient to generate an enhanced immune response to the nucleic acid vaccine. The adjuvant can be administered prior to (*e.g.*, 1 or more days before) inoculation with the nucleic acid vaccine; concurrently with (*e.g.*, within 24 hours of) inoculation with the nucleic acid vaccine; contemporaneously (simultaneously) with the nucleic acid vaccine (*e.g.*, the adjuvant is mixed with the nucleic acid vaccine, and the mixture is administered to the vertebrate); or after (*e.g.*, 1 or more days after) inoculation with the nucleic acid vaccine. The adjuvant can also be administered at more than one time (*e.g.*, prior to inoculation with the nucleic acid vaccine and also after inoculation with the nucleic acid vaccine). As used herein, the term "in conjunction with" encompasses any time period, including those specifically described herein and combinations of the time periods specifically described herein, during which the adjuvant can be administered so as to generate an enhanced immune response to the nucleic acid vaccine (*e.g.*, an increased antibody titer to the antigen encoded by the nucleic acid vaccine, or an

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increased antibody titer to *M. catarrhalis*). The adjuvant and the nucleic acid vaccine can be administered at approximately the same location on the vertebrate; for example, both the adjuvant and the nucleic acid vaccine are administered at a marked site on a limb of the vertebrate.

5 In a particular embodiment, the nucleic acid construct is co-administered with a transfection-facilitating agent. In a preferred embodiment, the transfection-facilitating agent is dioctylglycylspermine (DOGS) (as exemplified in published PCT application publication no. WO 96/21356 and incorporated herein by reference). In another embodiment, the transfection-facilitating agent is bupivacaine (as exemplified in U.S. Patent 5,593,972 and incorporated
10 herein by reference).

6.4 Animal Model for Testing Efficacy of Therapies

The evaluation of the functional significance of antibodies to surface antigens of *M. catarrhalis* has been hampered by the lack of a suitable animal model. The relative lack of virulence of this organism for animals rendered identification of an appropriate model system
15 difficult (Doern, 1986). Attempts to use rodents, including chinchillas, to study middle ear infections caused by *M. catarrhalis* were unsuccessful, likely because this organism cannot grow or survive in the middle ear of these hosts (Doyle, 1989).

Murine short-term pulmonary clearance models have now been developed (Unhanand *et al.*, 1992; Verghese *et al.*, 1990) which permit an evaluation of the interaction of *M. catarrhalis*
20 with the lower respiratory tract as well as assessment of pathologic changes in the lungs. This model reproducibly delivers an inoculum of bacteria to a localized peripheral segment of the murine lung. Bacteria multiply within the lung, but are eventually cleared as a result of (i) resident defense mechanisms, (ii) the development of an inflammatory response, and/or (iii) the development of a specific immune response. Using this model, it has been demonstrated that
25 serum IgG antibody can enter the alveolar spaces in the absence of an inflammatory response and enhance pulmonary clearance of nontypable *H. influenzae* (McGehee *et al.*, 1989), a pathogen with a host range and disease spectrum nearly identical to those of *M. catarrhalis*.

7.0 Screening Assays

In still further embodiments, the present invention provides methods for identifying new *M. catarrhalis* inhibitory compounds, which may be termed as "candidate substances," by screening for immunogenic activity with peptides that include one or more mutations to the identified immunogenic epitopic region. It is contemplated that such screening techniques will prove useful in the general identification of any compound that will serve the purpose of inhibiting, or even killing, *M. catarrhalis*, and in preferred embodiments, will provide candidate vaccine compounds.

It is further contemplated that useful compounds in this regard will in no way be limited to proteinaceous or peptidyl compounds. In fact, it may prove to be the case that the most useful pharmacological compounds for identification through application of the screening assays will be non-peptidyl in nature and, *e.g.*, which will serve to inhibit bacterial protein transcription through a tight binding or other chemical interaction. Candidate substances may be obtained from libraries of synthetic chemicals, or from natural samples, such as rain forest and marine samples.

To identify a *M. catarrhalis* inhibitor, one would simply conduct parallel or otherwise comparatively controlled immunoassays and identify a compound that inhibits the phenotype of *M. catarrhalis*. Those of skill in the art are familiar with the use of immunoassays for competitive screenings (for example refer to Sambrook *et al.* 1989).

Once a candidate substance is identified, one would measure the ability of the candidate substance to inhibit *M. catarrhalis* in the presence of the candidate substance. In general, one will desire to measure or otherwise determine the activity of *M. catarrhalis* in the absence of the added candidate substance relative to the activity in the presence of the candidate substance in order to assess the relative inhibitory capability of the candidate substance.

7.1 Mutagenesis

Site-specific mutagenesis is a technique useful in the preparation of individual peptides, or biologically functional equivalent proteins or peptides, through specific mutagenesis of the underlying DNA. The technique further provides a ready ability to prepare and test sequence

variants, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to 25 nucleotides in length is preferred, with about 5 to 10 residues on both sides of the junction of the sequence being altered.

In general, the technique of site-specific mutagenesis is well known in the art, as will be appreciated, the technique typically employs a bacteriophage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage vectors are commercially available and their use is generally well known to those skilled in the art. Double stranded plasmids are also routinely employed in site directed mutagenesis, which eliminates the step of transferring the gene of interest from a phage to a plasmid.

In general, site-directed mutagenesis is performed by first obtaining a single-stranded vector, or melting of two strands of a double stranded vector which includes within its sequence a DNA sequence encoding the desired protein. An oligonucleotide primer bearing the desired mutated sequence is synthetically prepared. This primer is then annealed with the single-stranded DNA preparation, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected that include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected gene using site-directed mutagenesis is provided as a means of producing potentially useful species and is not meant to be limiting, as there are other ways in which sequence variants of genes may be obtained. For

example, recombinant vectors encoding the desired gene may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants.

7.2 Second Generation Inhibitors

5 In addition to the inhibitory compounds initially identified, the inventor also contemplates that other sterically similar compounds may be formulated to mimic the key portions of the structure of the inhibitors. Such compounds, which may include peptidomimetics of peptide inhibitors, may be used in the same manner as the initial inhibitors.

10 Certain mimetics that mimic elements of protein secondary structure are designed using the rationale that the peptide backbone of proteins exists chiefly to orientate amino acid side chains in such a way as to facilitate molecular interactions. A peptide mimetic is thus designed to permit molecular interactions similar to the natural molecule.

15 Some successful applications of the peptide mimetic concept have focused on mimetics of β -turns within proteins, which are known to be highly antigenic. Likely β -turn structure within a polypeptide can be predicted by computer-based algorithms, as discussed herein. Once the component amino acids of the turn are determined, mimetics can be constructed to achieve a similar spatial orientation of the essential elements of the amino acid side chains.

20 The generation of further structural equivalents or mimetics may be achieved by the techniques of modeling and chemical design known to those of skill in the art. The art of computer-based chemical modeling is now well known. Using such methods, a chemical that specifically inhibits viral transcription elongation can be designed, and then synthesized,
25 following the initial identification of a compound that inhibits RNA elongation, but that is not specific or sufficiently specific to inhibit viral RNA elongation in preference to human RNA elongation. It will be understood that all such sterically similar constructs and second generation molecules fall within the scope of the present invention.

8.0 Diagnosing *M. catarrhalis* Infections

8.1 Amplification and PCR™

Nucleic acid sequence used as a template for amplification is isolated from cells contained in the biological sample, according to standard methodologies (Sambrook *et al.*, 1989). The nucleic acid may be genomic DNA or fractionated or whole cell RNA. Where RNA is used, it may be desired to convert the RNA to a cDNA.

Pairs of primers that selectively hybridize to nucleic acids corresponding to UspA1 or UspA2 protein or a mutant thereof are contacted with the isolated nucleic acid under conditions that permit selective hybridization. The term "primer", as defined herein, is meant to encompass any nucleic acid that is capable of priming the synthesis of a nascent nucleic acid in a template-dependent process. Typically, primers are oligonucleotides from ten to twenty base pairs in length, but longer sequences can be employed. Primers may be provided in double-stranded or single-stranded form, although the single-stranded form is preferred.

Once hybridized, the nucleic acid:primer complex is contacted with one or more enzymes that facilitate template-dependent nucleic acid synthesis. Multiple rounds of amplification, also referred to as "cycles," are conducted until a sufficient amount of amplification product is produced.

Next, the amplification product is detected. In certain applications, the detection may be performed by visual means. Alternatively, the detection may involve indirect identification of the product *via* chemiluminescence, radioactive scintigraphy of incorporated radiolabel or fluorescent label or even *via* a system using electrical or thermal impulse signals (Affymax technology).

A number of template dependent processes are available to amplify the marker sequences present in a given template sample. One of the best known amplification methods is the polymerase chain reaction (referred to as PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, and each incorporated herein by reference in entirety.

Briefly, in PCRTM, two primer sequences are prepared that are complementary to regions on opposite complementary strands of the marker sequence. An excess of deoxynucleoside triphosphates are added to a reaction mixture along with a DNA polymerase, *e.g.*, *Taq* polymerase. If the marker sequence is present in a sample, the primers will bind to the marker and the polymerase will cause the primers to be extended along the marker sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the marker to form reaction products, excess primers will bind to the marker and to the reaction products and the process is repeated.

A reverse transcriptase PCRTM (RT-PCRTM) amplification procedure may be performed in order to quantify the amount of mRNA amplified or to prepare cDNA from the desired mRNA. Methods of reverse transcribing RNA into cDNA are well known and described in Sambrook *et al.*, 1989. Alternative methods for reverse transcription utilize thermostable, RNA-dependent DNA polymerases. These methods are described in WO 90/07641, filed December 21, 1990, incorporated herein by reference. Polymerase chain reaction methodologies are well known in the art.

Another method for amplification is the ligase chain reaction ("LCR"), disclosed in EPA No. 320 308, incorporated herein by reference in its entirety. In LCR, two complementary probe pairs are prepared, and in the presence of the target sequence, each pair will bind to opposite complementary strands of the target such that they abut. In the presence of a ligase, the two probe pairs will link to form a single unit. By temperature cycling, as in PCRTM, bound ligated units dissociate from the target and then serve as "target sequences" for ligation of excess probe pairs. U.S. Patent 4,883,750 describes a method similar to LCR for binding probe pairs to a target sequence.

Qbeta Replicase, described in PCT Application No. PCT/US87/00880, incorporated herein by reference, may also be used as still another amplification method in the present invention. In this method, a replicative sequence of RNA that has a region complementary to that of a target is added to a sample in the presence of an RNA polymerase. The polymerase will copy the replicative sequence that can then be detected.

An isothermal amplification method, in which restriction endonucleases and ligases are used to achieve the amplification of target molecules that contain nucleotide 5'-[alpha-thio]-triphosphates in one strand of a restriction site may also be useful in the amplification of nucleic acids in the present invention.

Strand Displacement Amplification (SDA) is another method of carrying out isothermal amplification of nucleic acids which involves multiple rounds of strand displacement and synthesis, *i.e.*, nick translation. A similar method, called Repair Chain Reaction (RCR), involves annealing several probes throughout a region targeted for amplification, followed by a repair reaction in which only two of the four bases are present. The other two bases can be added as biotinylated derivatives for easy detection. A similar approach is used in SDA. Target specific sequences can also be detected using a cyclic probe reaction (CPR). In CPR, a probe having 3' and 5' sequences of non-specific DNA and a middle sequence of specific RNA is hybridized to DNA that is present in a sample. Upon hybridization, the reaction is treated with RNase H, and the products of the probe identified as distinctive products that are released after digestion. The original template is annealed to another cycling probe and the reaction is repeated.

Still another amplification methods described in GB Application No. 2 202 328, and in PCT Application No. PCT/US89/01025, each of which is incorporated herein by reference in its entirety, may be used in accordance with the present invention. In the former application, "modified" primers are used in a PCRTM-like, template- and enzyme-dependent synthesis. The primers may be modified by labeling with a capture moiety (*e.g.*, biotin) and/or a detector moiety (*e.g.*, enzyme). In the latter application, an excess of labeled probes are added to a sample. In the presence of the target sequence, the probe binds and is cleaved catalytically. After cleavage, the target sequence is released intact to be bound by excess probe. Cleavage of the labeled probe signals the presence of the target sequence.

Other nucleic acid amplification procedures include transcription-based amplification systems (TAS), including nucleic acid sequence based amplification (NASBA) and 3SR Gingeras *et al.*, PCT Application WO 88/10315, incorporated herein by reference. In NASBA, the nucleic acids can be prepared for amplification by standard phenol/chloroform extraction.

heat denaturation of a clinical sample, treatment with lysis buffer and minispin columns for isolation of DNA and RNA or guanidinium chloride extraction of RNA. These amplification techniques involve annealing a primer which has target specific sequences. Following polymerization, DNA/RNA hybrids are digested with RNase H while double stranded DNA molecules are heat denatured again. In either case the single stranded DNA is made fully double stranded by addition of second target specific primer, followed by polymerization. The double-stranded DNA molecules are then multiply transcribed by an RNA polymerase such as T7 or SP6. In an isothermal cyclic reaction, the RNA's are reverse transcribed into single stranded DNA, which is then converted to double stranded DNA, and then transcribed once again with an RNA polymerase such as T7 or SP6. The resulting products, whether truncated or complete, indicate target specific sequences.

Davey *et al.*, EPA No. 329 822 (incorporated herein by reference in its entirety) disclose a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA), which may be used in accordance with the present invention. The ssRNA is a template for a first primer oligonucleotide, which is elongated by reverse transcriptase (RNA-dependent DNA polymerase). The RNA is then removed from the resulting DNA:RNA duplex by the action of ribonuclease H (RNase H, an RNase specific for RNA in duplex with either DNA or RNA). The resultant ssDNA is a template for a second primer, which also includes the sequences of an RNA polymerase promoter (exemplified by T7 RNA polymerase) 5' to its homology to the template. This primer is then extended by DNA polymerase (exemplified by the large "Klenow" fragment of *E. coli* DNA polymerase I), resulting in a double-stranded DNA ("dsDNA") molecule, having a sequence identical to that of the original RNA between the primers and having additionally, at one end, a promoter sequence. This promoter sequence can be used by the appropriate RNA polymerase to make many RNA copies of the DNA. These copies can then re-enter the cycle leading to very swift amplification. With proper choice of enzymes, this amplification can be done isothermally without addition of enzymes at each cycle. Because of the cyclical nature of this process, the starting sequence can be chosen to be in the form of either DNA or RNA.

Miller *et al.*, PCT Application WO 89/06700 (incorporated herein by reference in its entirety) disclose a nucleic acid sequence amplification scheme based on the hybridization of a

promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. This scheme is not cyclic, *i.e.*, new templates are not produced from the resultant RNA transcripts. Other amplification methods include "RACE" and "one-sided PCR" (Frohman, 1990, incorporated by reference).

5

Methods based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide, may also be used in the amplification step of the present invention.

10

Following any amplification, it may be desirable to separate the amplification product from the template and the excess primer for the purpose of determining whether specific amplification has occurred. In one embodiment, amplification products are separated by agarose, agarose-acrylamide or polyacrylamide gel electrophoresis using standard methods. See Sambrook *et al.*, 1989.

15

Alternatively, chromatographic techniques may be employed to effect separation. There are many kinds of chromatography which may be used in the present invention: adsorption, partition, ion-exchange and molecular sieve, and many specialized techniques for using them including column, paper, thin-layer and gas chromatography.

20

Amplification products must be visualized in order to confirm amplification of the marker sequences. One typical visualization method involves staining of a gel with ethidium bromide and visualization under UV light. Alternatively, if the amplification products are integrally labeled with radio- or fluorometrically-labeled nucleotides, the amplification products can then be exposed to x-ray film or visualized under the appropriate stimulating spectra, following separation.

25

30

In one embodiment, visualization is achieved indirectly. Following separation of amplification products, a labeled, nucleic acid probe is brought into contact with the amplified marker sequence. The probe preferably is conjugated to a chromophore but may be radiolabeled. In another embodiment, the probe is conjugated to a binding partner, such as an antibody or biotin, and the other member of the binding pair carries a detectable moiety.

In one embodiment, detection is by Southern blotting and hybridization with a labeled probe. The techniques involved in Southern blotting are well known to those of skill in the art and can be found in many standard books on molecular protocols. See Sambrook *et al.*, 1989. Briefly, amplification products are separated by gel electrophoresis. The gel is then contacted with a membrane, such as nitrocellulose, permitting transfer of the nucleic acid and non-covalent binding. Subsequently, the membrane is incubated with a chromophore-conjugated probe that is capable of hybridizing with a target amplification product. Detection is by exposure of the membrane to x-ray film or ion-emitting detection devices.

One example of the foregoing is described in U.S. Patent No. 5,279,721, incorporated by reference herein, which discloses an apparatus and method for the automated electrophoresis and transfer of nucleic acids. The apparatus permits electrophoresis and blotting without external manipulation of the gel and is ideally suited to carrying out methods according to the present invention.

All the essential materials and reagents required for detecting P-TEFb or kinase protein markers in a biological sample may be assembled together in a kit. This generally will comprise preselected primers for specific markers. Also included may be enzymes suitable for amplifying nucleic acids including various polymerases (RT, Taq, *etc.*), deoxynucleotides and buffers to provide the necessary reaction mixture for amplification.

Such kits generally will comprise, in suitable means, distinct containers for each individual reagent and enzyme as well as for each marker primer pair. Preferred pairs of primers for amplifying nucleic acids are selected to amplify the sequences specified in SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16 such that, for example, nucleic acid fragments are prepared that include a contiguous stretch of nucleotides identical to for example about 15, 20, 25, 30, 35, *etc.*; 48, 49, 50, 51, *etc.*; 75, 76, 77, 78, 79, 80 *etc.*; 100, 101, 102, 103 *etc.*; 118, 119, 120, 121 *etc.*; 127, 128, 129, 130, 131, *etc.*; 316, 317, 318, 319, *etc.*; 322, 323, 324, 325, 326, *etc.*; 361, 362, 363, 364, *etc.*; 372, 373, 374, 375, *etc.* of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID

NO:16, so long as the selected contiguous stretches are from spatially distinct regions. Similar fragments may be prepared which are identical or complimentary to, for example, SEQ ID NO:1 such that the fragments do not hybridize to, for example, SEQ ID NO:3.

5 In another embodiment, such kits will comprise hybridization probes specific for UspA1 or UspA2 proteins chosen from a group including nucleic acids corresponding to the sequences specified in SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16 or to intermediate lengths of the sequences specified. Such kits generally will comprise, in suitable means, distinct containers
10 for each individual reagent and enzyme as well as for each marker hybridization probe.

8.2 Other Assays

 Other methods for genetic screening to accurately detect *M. catarrhalis* infections that alter normal cellular production and processing, in genomic DNA, cDNA or RNA samples may
15 be employed, depending on the specific situation.

 For example, one method of screening for genetic variation is based on RNase cleavage of base pair mismatches in RNA/DNA and RNA/RNA heteroduplexes. As used herein, the term "mismatch" is defined as a region of one or more unpaired or mispaired nucleotides in a
20 double-stranded RNA/RNA, RNA/DNA or DNA/DNA molecule. This definition thus includes mismatches due to insertion/deletion mutations, as well as single and multiple base point mutations.

 U.S. Patent No. 4,946,773 describes an RNase A mismatch cleavage assay that involves
25 annealing single-stranded DNA or RNA test samples to an RNA probe, and subsequent treatment of the nucleic acid duplexes with RNase A. After the RNase cleavage reaction, the RNase is inactivated by proteolytic digestion and organic extraction, and the cleavage products are denatured by heating and analyzed by electrophoresis on denaturing polyacrylamide gels. For the detection of mismatches, the single-stranded products of the RNase A treatment,
30 electrophoretically separated according to size, are compared to similarly treated control duplexes. Samples containing smaller fragments (cleavage products) not seen in the control duplex are scored as +.

Currently available RNase mismatch cleavage assays, including those performed according to U.S. Patent No. 4,946,773, require the use of radiolabeled RNA probes. Myers and Maniatis in U.S. Patent No. 4,946,773 describe the detection of base pair mismatches using
5 RNase A. Other investigators have described the use of *E. coli* enzyme, RNase I, in mismatch assays. Because it has broader cleavage specificity than RNase A, RNase I would be a desirable enzyme to employ in the detection of base pair mismatches if components can be found to decrease the extent of non-specific cleavage and increase the frequency of cleavage of mismatches. The use of RNase I for mismatch detection is described in literature from Promega
10 Biotech. Promega markets a kit containing RNase I that is shown in their literature to cleave three out of four known mismatches, provided the enzyme level is sufficiently high.

The RNase protection assay was first used to detect and map the ends of specific mRNA targets in solution. The assay relies on being able to easily generate high specific activity
15 radiolabeled RNA probes complementary to the mRNA of interest by *in vitro* transcription. Originally, the templates for *in vitro* transcription were recombinant plasmids containing bacteriophage promoters. The probes are mixed with total cellular RNA samples to permit hybridization to their complementary targets, then the mixture is treated with RNase to degrade excess unhybridized probe. Also, as originally intended, the RNase used is specific for single-
20 stranded RNA, so that hybridized double-stranded probe is protected from degradation. After inactivation and removal of the RNase, the protected probe (which is proportional in amount to the amount of target mRNA that was present) is recovered and analyzed on a polyacrylamide gel.

25 The RNase Protection assay was adapted for detection of single base mutations. In this type of RNase A mismatch cleavage assay, radiolabeled RNA probes transcribed *in vitro* from wild type sequences, are hybridized to complementary target regions derived from test samples. The test target generally comprises DNA (either genomic DNA or DNA amplified by cloning in plasmids or by PCRTM), although RNA targets (endogenous mRNA) have occasionally been
30 used. If single nucleotide (or greater) sequence differences occur between the hybridized probe and target, the resulting disruption in Watson-Crick hydrogen bonding at that position ("mismatch") can be recognized and cleaved in some cases by single-strand specific

ribonuclease. To date, RNase A has been used almost exclusively for cleavage of single-base mismatches, although RNase I has recently been shown as useful also for mismatch cleavage. There are recent descriptions of using the MutS protein and other DNA-repair enzymes for detection of single-base mismatches.

9.0 Examples

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

EXAMPLE I: Sequence Analysis and Characterization of *uspA1*

Bacterial strains and culture conditions. *M. catarrhalis* strains 035E, 046E, TTA24, 012E, FR2682, and B21 have been previously described (Helminen *et al.*, 1993a; Helminen *et al.*, 1994; Unhanand *et al.*, 1992). *M. catarrhalis* strains FR3227 and FR2336 were obtained from Richard Wallace, University of Texas Health Center, Tyler, TX. *M. catarrhalis* strain B6 was obtained from Elliot Juni, University of Michigan, Ann Arbor, MI. *M. catarrhalis* strain TTA1 was obtained from Steven Berk, East Tennessee State University, Johnson City, TN. *M. catarrhalis* strain 25240 was obtained from the American Type Culture Collection, Rockville, MD. *M. catarrhalis* strains were routinely cultured in Brain Heart Infusion (BHI) broth (Difco Laboratories, Detroit, MI) at 37°C or on BHI agar plates in an atmosphere of 95% air-5% CO₂. *Escherichia coli* strains LE392 and XL1-Blue MRF' (Stratagene, La Jolla, CA) were grown on Lubria-Bertani medium (Maniatis *et al.*, 1982) supplemented with maltose (0.2% w/v) and 10 mM MgSO₄ at 37°C, with antimicrobial supplementation as necessary.

Monoclonal antibodies (MAbs). MAb 17C7 is a murine IgG antibody reactive with the UspA proteinaceous material of all *M. catarrhalis* strains tested to date (Helminen *et al.*, 1994). Additional MAbs specific for UspA material (*i.e.*, 16A7, 17B1, and 5C12) were produced for this study by fusing spleen cells from mice immunized with outer membrane vesicles from

M. catarrhalis 035E with the SP2/0-Ag14 plasmacytoma cell line, as described (Helminen *et al.*, 1993a). These MAbs were used in the form of hybridoma culture supernatant fluid in western blot and dot blot analyses.

Cloning vectors. Plasmid and bacteriophage cloning vectors utilized in this work and the recombinant derivatives of these vectors are listed in Table VI.

TABLE VI
Bacteriophages And Plasmids

Bacteriophage or plasmid	Description	Source
Bacteriophage		
LambdaGEM-11	Cloning vector	Promega Corp. (Madison, WI)
MEH200	LambdaGEM-11 containing an 11 kb insert of <i>M. catarrhalis</i> strain 035E DNA encoding the UspA proteinaceous material	(Helminen <i>et al.</i> , 1994)
ZAP Express	Cloning vector	Stratagene
USP100	ZAP Express with a 2.7 kb fragment of DNA (containing the <i>uspA1</i>) amplified from the chromosome of <i>M. catarrhalis</i> strain 035E	This study
Plasmids		
pBluescript II SK+ (pBS)	Cloning vector, Amp ^R	Stratagene
pJL501.6	pBS containing the 1.6 kb <i>Bgl</i> II- <i>Eco</i> RI fragment from MEH200	This study
pJL500.5	pBS containing the 600-bp <i>Bgl</i> II fragment from MEH200	This study

MEH200, the original recombinant bacteriophage clone that produced plaques reactive with the UspA-specific MAb 17C7, has been described previously (Helminen *et al.*, 1994).

Genetic techniques. Standard recombinant DNA techniques including plasmid isolation, restriction enzyme digestions, DNA modifications, ligation reactions and transformation of *E. coli* are familiar to those of skill in the art and were performed as previously described (Maniatis *et al.*, 1982; Sambrook *et al.*, 1989).

Polymerase Chain Reaction (PCRTM). PCRTM was performed using the GeneAmp kit (Perkin-Elmer, Branchburg, NJ). All reaction were carried out according to the manufacturer's instructions. To amplify products from total genomic DNA, 1 µg of *M. catarrhalis* chromosomal DNA and 100 ng of each primer were used in each 100 µl reaction.

Nucleotide sequence analysis. Nucleotide sequence analysis of DNA fragments in recombinant plasmids, in bacteriophage, or derived by PCRTM was performed using an Applied Biosystems Model 373A automated DNA sequencer (Applied Biosystems, Foster City, CA). DNA sequence information was analyzed using the Intelligenetics suite package and programs from the University of Wisconsin Genetics Computer Group software analysis package (Devereux *et al.*, 1984). Analysis of protein hydrophilicity using the method of Kyte and Doolittle (1982) and analysis of repeated amino acid sequences within the UspA protein was performed using the MacVectorTM software protein matrix analysis package (Eastman Kodak Company, Rochester, NY).

Identification of recombinant bacteriophage. Lysates were generated from *E. coli* cells infected with recombinant bacteriophage by using the plate lysis method as described (Helminen *et al.*, 1994). MAb-based screening of plaques formed by recombinant ZAP Express bacteriophage on *E. coli* XL1-Blue MRF' cells was performed according to the manufacturer's instructions (Stratagene, La Jolla, CA). Briefly, nitrocellulose filters soaked in 10 mM IPTG were applied to the surface of agar plates five hours after bacteriophage infection of the bacterial lawn. After overnight incubation at 37°C, the nitrocellulose pads were removed, washed with PBS containing 0.5% (v/v) Tween 20 and 5% (w/v) skim milk (PBS-T) and incubated with hybridoma culture supernatant containing the MAb for 4 hours at room temperature. After four washes with PBS-T, PBS-T containing ¹²⁵I-labeled goat anti-mouse

IgG was applied to each pad. After overnight incubation at 4°C, the pads were washed four times with PBS-T, blotted dry, and exposed to film.

Characterization of *M. catarrhalis* protein antigens. Outer membrane vesicles were prepared from BHI broth-grown *M. catarrhalis* cells by the EDTA-buffer method (Murphy and Loeb, 1989). Proteins present in these vesicles were resolved by sodium dodecyl sulfate (SDS)-polyacrylamide gel electrophoresis (PAGE) using 7.5% (w/v) polyacrylamide separating gels. These SDS-PAGE-resolved proteins were electrophoretically transferred to nitrocellulose and western blot analysis was performed as described using MAb 17C7 as the primary antibody (Kimura *et al.*, 1985). For western blot analysis of proteins encoded by DNA inserts in recombinant bacteriophage, one part of a lysate from bacteriophage-infected *E. coli* cells was mixed with one part SDS-digestion buffer (Kimura *et al.*, 1985) and this mixture was incubated at 37°C for 15 minutes prior to SDS-PAGE.

Features of the *uspA1* gene and its encoded protein product. The nucleotide sequence of the *M. catarrhalis* 035E *uspA1* gene and the deduced amino acid sequence of the UspA1 protein are provided in SEQ ID NO:2 and SEQ ID NO:1, respectively. The open reading frame (ORF), containing 2,493 nucleotides, encoded a protein product of 831 amino acids, with a calculated molecular mass of 88,271 daltons.

The predicted protein product of the *uspA1* ORF had a pI of 4.7, was highly hydrophilic, and was characterized by extensively repeated motifs. The first motif consists of the consensus sequence NXAXXYSXIGGGXN (SEQ ID NO:24), which is extensively repeated between amino acid residues 80 and 170. The second region, from amino acid residues 320 to 460, contains a long sequence which is repeated three times in its entirety, but which also contains smaller units which are repeated several times themselves. This "repeat within a repeat" arrangement is also true of the third region, which extends from amino acid residues 460 to 600. This last motif consists of many repeats of the small motif QADI (SEQ ID NO:25) and two large repeats which contain the QADI (SEQ ID NO:25) motif within themselves.

Similarity of UspA1 to other proteins. A BLAST-X search (Altschul *et al.*, 1990; Gish and States, 1993) of the available databases for proteins with significant homology to UspA1 indicated that the prokaryotic proteins that were most similar to this *M. catarrhalis* antigen were

a putative adhesin of *H. influenzae* Rd (GenBank accession number U32792) (Fleischmann *et al.*, 1995), the Hia adhesin from nontypable *H. influenzae* (GenBank accession number U38617) (Barenkamp and St. Geme III, 1996), and the YadA invasin of *Yersinia enterocolitica* (Skurnik and Wolf-Watz, 1989) (SwissProt:P31489). When the GAP alignment program (Devereux *et al.*, 1984) was used to compare the UspA1 sequence to that of these and closely related bacterial adhesins, UspA1 proved to be 25% identical and 47% similar to the *E. coli* AIDA-I adhesin from enteropathogenic *E. coli* (Benz and Schmidt, 1989; Benz and Schmidt, 1992b), 23% identical and 46% similar to Hia (Barenkamp and St. Geme III, 1996), and 24% identical and 43% similar to YadA (Skurnik and Wolf-Watz, 1989). Other proteins retrieved from database searches as having homology with UspA1 included myosin heavy chains from a number of species.

EXAMPLE II: Two Genes Encode the Proteins UspA1 and UspA2

MAb 17C7 binds to a very high molecular weight proteinaceous material of *M. catarrhalis*, designated UspA, that migrates with an apparent molecular weight (in SDS-PAGE) of at least 250 kDa. This same MAb also reacts with another antigen band of approximately 100 kDa, as described in U.S. Patent No. 5,552,146 and incorporated herein by reference, and it is bound by a phage lysate from *E. coli* infected by a recombinant bacteriophage that contained a fragment of *M. catarrhalis* chromosomal DNA. The *M. catarrhalis* proteinaceous material in the phage lysate that binds this MAb migrates at a rate similar or indistinguishable from that of the native UspA material (Helminen *et al.*, 1994).

Analysis of *uspA1*. Nucleotide sequence analysis of the *M. catarrhalis* strain O35E gene expressed by the recombinant bacteriophage, designated *uspA1*, revealed the presence of an ORF encoding a predicted protein product with a molecular mass of 88,271 (SEQ ID NO:1). The use of the *uspA1* ORF in an *in vitro* DNA-directed protein expression system revealed that the protein encoded by the *uspA1* gene migrated in SDS-PAGE with an apparent molecular weight of about 120 kDa. (Those of skill in the art will be aware that denaturing processes, such as SDS-PAGE, can alter the migration rate of proteins such that the apparent molecular weight of the denatured protein is somewhat different than the predicted molecular weight of the non-denatured protein.) In addition, when the *uspA1* ORF was introduced into a bacteriophage vector, the recombinant *E. coli* strain containing this recombinant phage expressed a protein that migrated in SDS-PAGE apparently at the same rate as the native UspA protein from *M. catarrhalis*.

Southern blot analysis of chromosomal DNA from several *M. catarrhalis* strains, using a 0.6 kb *BglII-PvuII* fragment derived from the cloned *uspA1* gene as the probe, revealed that, with several strains, there were two distinct restriction fragments that bound this *uspA1*-derived probe (FIG. 1), indicating that *M. catarrhalis* possessed a second gene had some similarity to the *uspA1* gene.

Native very high molecular weight UspA proteinaceous material from *M. catarrhalis* strain O35E was resolved by SDS PAGE, electroeluted, and digested with a protease. N-terminal acid sequence analysis of some of the resultant peptides revealed that the amino acid sequences of several peptides did not match that of the deduced amino acid sequence of UspA1. Other peptides obtained from this experiment were similar to those present in the deduced amino acid sequence but not identical.

Protease and cyanogen bromide (CNBr) Cleavage of High Molecular Weight UspA Proteinaceous Material: Three tenths (0.3) mg of purified very high molecular weight UspA proteinaceous material (at the time of the purification this material was thought to be a single protein) was precipitated with 90% ethanol and the pellet was resuspended in 100 ml of 88% formic acid containing 12M urea. Following resuspension, 100 ml of 88% formic acid containing 2M CNBr was added and the mixture was incubated in the dark overnight at room temperature. One ml (2.0 mg) of purified UspA material was added directly to a vial containing 25 mg of either trypsin or chymotrypsin. The reaction mixtures were incubated for ~48 hours at 37°C. One ml (2.0 mg) of purified UspA material was added directly to a vial containing 15 mg of endoproteinase Lys-C. The reaction mixtures were incubated for about 48 hours at 37°C.

The cleavage reaction mixtures were clarified by centrifugation in an Eppendorf™ centrifuge at 12,000 rpm for 5 minutes. The clarified supernatant was loaded directly onto a Vydac C4 HPLC column using a mobile phase of 0.1% (v/v) aqueous trifluoroacetic acid (Solvent A) and acetonitrile:H₂O:trifluoroacetic acid, 80:20:0.1 (v/v/v) (Solvent B) at a flow rate of 1.0 ml/min. The reaction mixtures were washed onto the column with 100% Solvent A followed by elution of cleavage fragments using a 30 minutes linear gradient (0-100%) of Solvent B. Fractions were collected manually, dried overnight in a Speed-Vac and resuspended

in House Pure Water. The resuspended HPLC-separated fractions were subjected to SDS-PAGE analysis using 10-18% gradient gels in a Tris-Tricine buffer system. The fractions which exhibited a single peptide band were submitted for direct N-terminal sequence analysis. Fractions displaying multiple peptide bands were transferred from SDS-PAGE onto a PVDF
5 membrane and individual bands excised and submitted for N-terminal sequence analysis.

The N-terminal amino acid sequences of these fragments then were determined using an Applied Biosystems Model 477A PTH Analyzer (Applied Biosystems, Foster City, CA, U.S.A.). A summary of these sequences is given in Table VII. About half of the sequences
10 were found to match the sequence deduced from the *uspA1* gene, while the other half did not. Attempts at shifting the reading frame of the *uspA1* gene sequence failed to account for the non-matching peptide sequences, indicating that the high molecular weight UspA protein may comprise either a multimer of more than one distinct protein or distinct multimers of two different proteins.

TABLE VII

Summary of the N-terminal Sequences of Internal Peptide Fragments

Digest	Sequence ^a
CNBr	AAQAALSGLFVPYSVGKFNATAALGGYGSK SEQ ID NO:26 GKITKNAARQENG SEQ ID NO:27
LysC Digest #1	VIGDLGRKV SEQ ID NO:28 ALEXNVEEGL SEQ ID NO:29 ALESNVEEGLXXLS SEQ ID NO:30 ALEFNGE SEQ ID NO:31
LysC Digest #2	SITDLGXKV SEQ ID NO:32 SITDLGTIVDGFXXX SEQ ID NO:33 SITDLGTIVD SEQ ID NO:34
Trypsin	VDALXTKVNALDXKVNSDXT SEQ ID NO:35 LLAEQQLNGKTLTPV SEQ ID NO:36 AKHDAASTEKGKMD SEQ ID NO:37 ALESNVEEGLLDLSG SEQ ID NO:38
Trypsin Digest #1	NQNTLIEKTANK SEQ ID NO:39 IDKNEYSIK SEQ ID NO:40 SITDLGTK SEQ ID NO:41

TABLE VII (Continued)

Digest	Sequence ^a
Trypsin Digest #2	NQNTLIEK SEQ ID NO:42 ALHEQQLETLTK SEQ ID NO:43 NSSD SEQ ID NO:44 NKADADASFETLTK SEQ ID NO:45 FAATAIAKDK SEQ ID NO:46 KASSENTQNIK SEQ ID NO:47 RLLDQK SEQ ID NO:48
Chymotrypsin	AATADAITKNGX SEQ ID NO:49 AKAXAANXDR SEQ ID NO:50
Digest of research grade UspA with cys-C- endopeptidase	NQADIAQNQTDIQDLAAYNELQ SEQ ID NO:51 NQADIANNINNIYELAQQQDQ SEQ ID NO:52 YNERQTEAIDALN SEQ ID NO:53 ILGDTAIVSNSQD SEQ ID NO:54

^a Certain residues of several peptides could not be verified and these ambiguities are shown by an "X" in SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:49 and SEQ ID NO:50. In SEQ ID NO:29 the ambiguous residue is likely to be a serine; in SEQ ID NO:33, position 13 is likely to be aspartic acid, position 14 is likely to be glycine and position 15 is likely to be arginine; in SEQ ID NO:35 both positions 13 and 19 are likely to be serines; in SEQ ID NO:49 the ambiguous residue is likely to be an asparagine; and in SEQ ID NO:50 position 4 is likely to be serine and position 8 is likely to be threonine.

Additional attempts to resolve the very high molecular weight UspA protein band from *M. catarrhalis* strain O35E by SDS-PAGE, followed by electroelution and digestion with proteases or with cyanogen bromide, again yielded a number of peptides which were sequenced. Several peptides (peptides 1-6, Table VIII) were obtained. The amino acid sequence of which was identical or very similar to that deduced from the nucleotide sequence of the *uspA1* gene. However, several additional peptides, peptides 7-10, Table VIII, were not present in the deduced amino acid sequence. This finding substantiated the suggestion that a second protein was present in the UspA antigen preparation.

TABLE VIII

Matching or closely matching peptides:		
Peptide #	Amino acid sequence	
Peptide 1	KALESNVEEGLLDLSGR	(SEQ ID NO:55)
Peptide 2	ALESNVEEGLLELSGRTIDQR	(SEQ ID NO:56)
Peptide 3	NQAHIANINXIYELAQQQDQK	(SEQ ID NO:57)
Peptide 4	NQADIAQNQTDIQDLAAYNELQ	(SEQ ID NO:58)
Peptide 5	ATHDYNERQTEA	(SEQ ID NO:59)
Peptide 6	KASSENTQNIK	(SEQ ID NO:60)
Nonmatching peptides:		
Peptide #	Amino acid sequence	
Peptide 7	MILGDTAIVSNSQDNKTQLKFYK	(SEQ ID NO:61)
Peptide 8	AGDTIPLDDDDXXP	(SEQ ID NO:62)
Peptide 9	LLHEQQLXGK	(SEQ ID NO:63)
Peptide 10	IFFNXG	(SEQ ID NO:64)

^a Certain residues of several peptides could not be verified and these ambiguities are shown by an "X" in SEQ ID NO:57, SEQ ID NO:62, SEQ ID NO:63 and SEQ ID NO:64.

Further evidence corroborating the assertion that the high molecular weight UspA proteinaceous material was either a multimer of more than one distinct protein or distinct multimers of two different proteins was derived from earlier electrospray mass spectroscopic analysis which predicted that a monomer of the UspA material had a molecular weight of 59,500. This approximately 60 kDa protein reacted immunogenically with the MAbs 17C7, 45-2, 13-1, and 29-31, in contrast to the UspA1 protein which only cross-reacted with MAb 17C7. The fact that MAb 17C7 reacted with both isolated proteins suggested that this Mab recognized an epitope common to both proteins.

Preparation of mutant *uspA1* construct. The nucleotide sequence of the cloned *uspA1* gene was used to construct an isogenic *uspA1* mutant. Oligonucleotide primers (*Bam*HI-ended P1 and P16 in Table IX) were used to amplify a truncated version of the *uspA1* ORF from *M. catarrhalis* strain O35E chromosomal DNA; this PCRTM product was cloned into the *Bam*HI site of the

plasmid vector pBluescript II SK+. A 0.6 kb *Bgl*II fragment from the middle of this cloned fragment was excised and was replaced by a *Bam*HI-ended cassette encoding kanamycin resistance. This new plasmid was grown in *E. coli* DH5 α , purified by column chromatography, linearized by digestion with *Eco*RI, precipitated, and then dissolved in water. This linear DNA molecule was used to electroporate the wild-type *M. catarrhalis* strain O35E, using a technique described previously (Helminen *et al.*, 1993b). Approximately 5,000 kanamycin-resistant transformants were obtained; several picked at random were found to be still reactive with MAb 17C7. One of these kanamycin-resistant clones was randomly chosen for further examination and Southern blot analysis confirmed that this mutant was isogenic.

Analysis of products expressed by the *uspA1* mutant When whole cell lysates of both the wild-type *M. catarrhalis* strain and this mutant were subjected to SDS-PAGE, both the wild-type strain and the mutant strain still expressed the very high-molecular-weight band originally designated as UspA. However, a protein of approximately 120 kDa was found to be missing in the mutant strain (FIG. 2A). The fact that both this mutant and the wild-type parent strain still expressed a very high molecular weight antigen reactive with MAb 17C7 (FIG. 2B) indicated that there had to be a second gene in *M. catarrhalis* strain O35E that encoded a MAb 17C7-reactive antigen. Furthermore, it should be noted that EDTA-extracted outer membrane vesicles of both the wild-type strain (FIG. 2C, lanes 5 and 7) and mutant strain (FIG. 2C, lanes 6 and 8) possessed a protein of approximately 70-80 kDa that was reactive with MAb 17C7. This approximately 70-80 kDa band likely represents one form, perhaps the monomeric form, of the product of a second gene encoding the MAb 17C7-reactive epitope.

It is important to note that, when chromosomal DNA from both the wild-type parent strain and the mutant were digested with *Pvu*II and probed in Southern blot analysis with a 0.6 kb *Bgl*II-*Pvu*II fragment derived from the *uspA1* gene, the wild-type strain exhibited a 2.6 kb band and a 2.8 kb band which bound this probe (FIG. 3). In contrast, the mutant strain had a 2.6 kb band and a 3.4 kb band that bound this probe. The presence of the 3.4 kb band was the result of the insertion of the *kan* cartridge into the deletion site in the *uspA1* gene.

EXAMPLE III: Characterization of UspA2 and *uspA2*

Construction of fusion proteins. The epitope which binds MAb 17C7 was localized by using the nucleotide sequence of the *uspA1* gene described above to construct fusion proteins.

5 First, fusion proteins containing five peptides spanning the UspA1 protein were constructed by using the pGEX4T-2 protein fusion system (Pharmacia LKB). The oligonucleotide primers used in PCR™ to amplify the desired nucleotide sequences from *M. catarrhalis* strain O35E chromosomal DNA are listed in Table IX. Each of these had either a *Bam*HI site or a *Xho*I site at the 5' end, thereby allowing directional in-frame cloning of the amplified product into the

10 *Bam*HI- and *Xho*I-digested vector. When recombinant *E. coli* strains expressing each of these five fusion proteins were used in a colony blot radioimmunoassay, only fusion protein MF-4 readily bound MAb 17C7. Further analysis of the *uspA1*-derived nucleotide sequence in the MF-4 fusion construct involved the production of fusion proteins containing 79 amino acid residues (MF-4-1) and 123 amino acid residues (MF-4-2) derived from the MF-4 fusion protein

15 (Table IX). These two fusion proteins both bound MAb 17C7 (Table IX). FIG. 4 depicts the western blot reactivity of MAb 17C7 with the MF-4-1 fusion protein. These two fusion proteins had in common only a 23-residue region NNINNIYELAQQQDQHSSDIKTL (SEQ ID NO:65), suggesting that this 23-residue region, designated as the "3Q" peptide, contains the epitope that binds MAb 17C7.

TABLE IX

PCRTM primers used for the production of *usp A1* gene fragments for use in the construction of fusion proteins and mutagenesis and the reactivity of the resulting fusion protein with MAb 17C7

Fragment Generated:	Primer Pair ^a	Reactivity with MAb 17C7
MF-3	P5-P8	-
MF-4	P6-P13	+
MF-4.1	P7-P12	+
MF-4.2	P11-P13	+

5 ^a primer sequences are as follows:

P5	GGTGCAGGTCAGATCAGTGAC	SEQ ID NO:66
P6	GCCACCAACCAAGCTGAC	SEQ ID NO:67
P7	AGCGGTCGCCTGCTTGATCAG	SEQ ID NO:68
P8	CTGATCAAGCAGGCGACCGCT	SEQ ID NO:69
10 P11	CAAGATCTGGCCGCTTACAA	SEQ ID NO:70
P12	TTGTAAGCGGCCAGATCTTG	SEQ ID NO:71
P13	TGCATGAGCCGCAAACCC	SEQ ID NO:72

15 Elucidation of the MAb 17C7 Epitope. It is important to note that the nucleotide sequence encoding this 23-residue polypeptide (*i.e.*, the 3Q peptide) was present in the 0.6 kb *Bgl*III-*Pvu*II fragment used in the Southern blot analysis described in Example II. This finding suggested that the epitope that bound MAb 17C7 might be encoded by DNA present in both the 2.6 and 2.8 kb *Pvu*II fragments, with the 2.8 kb *Pvu*II fragment being derived from the cloned *uspA1* gene and the 2.6 kb *Pvu*II fragment representing all or part of another gene encoding this same epitope.

20 A ligation-based PCRTM system was used to verify this finding. Chromosomal DNA from the mutant strain was digested to completion with *Pvu*II and was resolved by agarose gel electrophoresis. Fragments ranging in size from 2-3 kb were excised from the agarose, blunt-ended, and ligated into the *Eco*RV site in pBluescript II SK+. This ligation reaction mixture was precipitated and used in a PCRTM amplification reaction. Each PCRTM reaction contained either the T3 or T7 primer derived from the DNA encoding the 3Q peptide. This approach yielded a 1.7

kb product with the T3 and P10 primers and a 0.9 kb product from the T7 and P9 primers (FIG. 5). The sum of these two bands is the same as the 2.6 kb size of the desired DNA fragment.

Nucleotide sequence analysis of these two PCRTM products revealed two incomplete ORFs which, when joined at the region encoding the 3Q peptide, formed a 1,728-bp ORF encoding a protein with a calculated molecular weight of 62,483 daltons (SEQ ID NO:3). The amino acid sequence of this protein had 43% identity with that of UspA1. Closer examination revealed that a region extending from amino acids 278-411 in this second protein, designated UspA2, was nearly identical to the region in UspA1 between amino acids 505-638 (SEQ ID NO:1). Furthermore, these two regions both contain the 23-mer (the 3Q peptide) that likely contains the epitope that binds MAb 17C7. It should also be noted that the four peptides from Table IX (Peptides 7-10) that were not found in UspA1 were found to be identical or very similar to peptides in the deduced amino acid sequence of UspA2. In addition, the first six peptides listed in Table IX, which matched or were very similar to peptides in the deduced amino acid sequence of UspA1, also matched peptides found in the deduced amino acid sequence of UspA2.

Oligonucleotide primers P1 and P2 (Table IX) were used to amplify a 2.5-2.6 kb fragment from *M. catarrhalis* strain O35E chromosomal DNA. Nucleotide sequence analysis of this PCRTM product was used to confirm the nucleotide sequence of the *uspA2* ORF determined from the ligation-based PCRTM study. These results proved that *M. catarrhalis* strain O35E contains two different ORFs (*i.e.*, *uspA1* and *uspA2*) which encode the same peptide (*i.e.*, the 3Q peptide) which likely binds MAb 17C7. This 3Q peptide appears twice in UspA1 and once in UspA2 (SEQ ID NO:1 and SEQ ID NO:3).

The nucleotide sequences of the two DNA segments encoding these 3Q peptides in *uspA1* are nearly identical, with three nucleotides being different. These nucleotide differences did not cause a change in the amino acid sequence. The nucleotide sequence of the DNA segment encoding the 3Q peptide in *uspA2* is identical to the DNA encoding the first 3Q peptide in UspA1.

As seen in FIG. 2C, lane 7, the three dominant MAb 17C7-reactive bands present in *M. catarrhalis* strain O35E outer membrane vesicles have apparent molecular weights of greater than 200 kDa, approximately 120 kDa, and approximately 70-80 kDa. It should be noted that the existence of several MAb 17C7-reactive bands, with apparent molecular weights of greater than 200 kDa, approximately 120 kDa, and approximately 70-80 kDa was also apparent in U.S. Patent

5,552,146 (FIG. 1, lane H). Therefore, the existence of at least more than one *M. catarrhalis* antigens reactive with MAb 17C7 was apparent as early as 1991. It is now apparent that the approximately 120 kDa band likely represents the monomeric form of the UspA1 antigen and the approximately 70-80 kDa band likely represents the monomeric form of the UspA2 antigen from *M. catarrhalis* strain O35E. One or more than one of these species may aggregate to form the very high molecular weight proteinaceous material (*i.e.* greater than 200 kDa) of the UspA antigen.

A new *M. catarrhalis* strain O35E genomic library was constructed in the bacteriophage vector ZAP Express (Stratagene, La Jolla, CA). Chromosomal DNA from this strain was partially digested with *Sau*3A1 and 4-9 kb DNA fragments were ligated into the vector arms according to the instructions obtained from the manufacturer. This library was amplified in *E. coli* MRF'. An aliquot of this library was diluted and plated and the resultant plaques were screened for reactivity with MAb 17C7. Approximately 24 plaques which bound this MAb were detected; the responsible recombinant bacteriophage were purified by the single plaque isolation method, and the DNA insert from one of these bacteriophage was subjected to nucleotide sequence analysis. Nucleotide sequence of the 2.6 kb DNA fragment present in this recombinant bacteriophage revealed that, on one end, it contained an incomplete ORF that encoded the 3Q peptide. Until its truncation by the vector cloning site, the sequence of this incomplete ORF was identical or nearly identical to that of the *uspA2* ORF derived from the ligation-based PCR™ study described immediately above, providing further evidence that two genes which share a common epitope encode the UspA antigen.

EXAMPLE IV: Purification of and Immunological Properties of the Proteins UspA1 and UspA2

Materials and Methods

Bacteria. TTA24 and O35E isolates were as previously described in Example I. Additional isolates were obtained from the University of Rochester and the American Type Culture Collection (ATCC). The bacteria were routinely passaged on Mueller-Hinton agar (Difco, Detroit, MI) incubated at 35°C with 5% carbon dioxide. The bacteria used for the purification of the protein were grown in sterile broth containing 10 g casamino acids (Difco, Detroit, MI) and 15 g yeast extract (BBL, Cockeysville, MD) per liter. The isolates were stored at -70°C in Mueller-Hinton broth containing 40% glycerol.

Purification of UspA2. Bacterial cells (~400 g wet wt. of *M. catarrhalis* O35E) were washed twice with 2 liters of pH 6.0, 0.03 M sodium phosphate (NaPO_4) containing 1.0% Triton[®] X-100 (TX-100) (J.T. Baker Inc., Philipsburg, NJ) (pH 6.0) by stirring at room temperature for 60 min. Cells containing the UspA2 protein were pelleted by centrifugation at 13,700 \times g for 30 min at 4°C. Following centrifugation, the pellet was resuspended in 2 liters of pH 8.0, 0.03 M Tris(hydroxymethyl)aminomethane-HCl (Tris-HCl) containing 1.0% TX-100 and stirred overnight at 4°C to extract the UspA2 protein. Cells were pelleted by centrifugation at 13,700 \times g for 30 min at 4°C. The supernatant, containing the UspA2 protein, was collected and further clarified by sequential microfiltration through a 0.8 μm membrane (CN.8, Nalge, Rochester, NY) then a 0.45 μm membrane (cellulose acetate, low protein binding, Corning, Corning, NY).

The entire filtered crude extract preparation was loaded onto a 50 \times 217 mm (~200 ml) TMAE column [650(S), 0.025-0.4 mm, EM Separations, Gibbstown, NJ] equilibrated with pH 8.0, 0.03 M Tris-HCl buffer containing 0.1% TX-100 (THT). The column was washed with 400 ml of equilibration buffer followed by 600 ml of 0.25 M NaCl in 0.03 M THT. UspA2 was subsequently eluted with 800 ml of 1.0 M NaCl in 0.03 M THT. Fractions were screened for UspA2 by SDS-PAGE and pooled. Pooled fractions (~750 ml), containing UspA2, were concentrated approximately two-fold by ultrafiltration using an Amicon stirred cell (Amicon Corp., Beverly, MA) with a YM-100 membrane under nitrogen pressure. The TMAE concentrate was split into two 175 ml aliquots and each aliquot buffer exchanged by passage over a 50 \times 280 mm (~550 ml) Sephadex G-25 (Coarse) column (Pharmacia Biotech, Piscataway, NJ) equilibrated with pH 7.0, 10 mM NaPO_4 containing 0.1% TX-100 (10 mM PT). The buffer exchanged material was subsequently loaded onto a 50 \times 217 mm (~425 ml) ceramic hydroxyapatite column (Type I, 40 μm , Bio-Rad) equilibrated with 10 mM PT. The column was washed with 450 ml of the equilibration buffer followed by 900 ml of pH 7.0, 0.1M NaPO_4 containing 0.1% TX-100. UspA2 was then eluted with a linear pH 7.0 NaPO_4 concentration gradient between 0.1 and 0.2 M NaPO_4 containing 0.1% TX-100. An additional volume of pH 7.0, 0.2 M NaPO_4 containing 0.1% TX-100 was applied to the column and collected to maximize the recovery of UspA2. Fractions were screened for UspA2 by SDS-PAGE and pooled. The column was then washed with 900 ml of pH 7.0, 0.5 M NaPO_4

containing 0.1% TX-100. The fractions from this wash were screened for UspA1 by SDS-PAGE, pooled, and stored at 4°C. This pool was used for the purification of UspA1.

Purification of UspA1. The UspA1 enriched fractions collected during four separate purifications of UspA2 were pooled. The combined UspA1 pools were concentrated approximately threefold by ultrafiltration using an Amicon stirred cell with a YM-100 membrane under nitrogen pressure. The UspA1 concentrate was split into two 175 ml aliquots and the buffer exchanged by passage over a 50 × 280 mm (~550 ml) Sephadex G-25 column equilibrated with 10 mM PT. The buffer exchanged material was subsequently loaded onto a 50 × 217 mm (~425 ml) ceramic hydroxyapatite column (Bio-Rad) equilibrated with 10 mM PT. The column was washed with 450 ml of the equilibration buffer followed by 900 ml of pH 7.0, 0.25 M NaPO₄ containing 0.1% TX-100. UspA1 was subsequently eluted with a linear NaPO₄ gradient of pH 7.0, 0.25-0.5 M NaPO₄ containing 0.1% TX-100. The fractions containing UspA1 were identified by SDS-PAGE and pooled.

SDS-PAGE and Western blot Analysis. SDS-PAGE was carried out as described by Laemmli (1970) using 4 to 20% (w/v) gradient acrylamide gels (Integrated Separation Systems (ISS), Natick, MA). Proteins were visualized by staining the gels with Coomassie Brilliant Blue R250. Gels were scanned using a Personal Densitometer SI (Molecular Dynamics Inc., Sunnyvale, CA) and molecular weights were estimated with the Fragment Analysis software (version 1.1) using the prestained molecular weight markers from ISS as standards. Transfer of proteins to polyvinylidene difluoride (PVDF) membranes was accomplished with a semi-dry electroblotter and electroblot buffers (ISS). The membranes were probed with protein specific antisera or MAb's followed by goat anti-mouse alkaline phosphatase conjugate as the secondary antibody (BioSource International, Camarillo, CA). Western blots were developed with the BCIP/NBT Phosphatase Substrate System (Kirkegaard and Perry Laboratories, Gaithersburg, MD).

Protein Estimation. Protein concentrations were estimated by the BCA assay (Pierce, Rockford, IL), using bovine serum albumin as the standard.

Enzymatic and Chemical Cleavages of UspA2 and UspA1.

(i) CNBr Cleavage. Approximately 0.3 mg of the purified protein was precipitated with 90% (v/v) ethanol and the pellet resuspended in 100 μ l of 88% (v/v) formic acid containing 12 M urea. Following resuspension, 100 μ l of 88% (v/v) formic acid containing 2 M CNBr (Sigma, St. Louis, MO) was added and the mixture incubated overnight at room temperature in the dark.

(ii) Trypsin and Chymotrypsin Cleavage. Approximately 2 mg of the purified protein was precipitated with 90% (v/v) ethanol and the pellet resuspended in a total volume of 1 ml of phosphate-buffered saline (PBS) containing 0.1% TX-100. This preparation was added directly to a vial containing 25 μ g of either trypsin or chymotrypsin (Boehringer Mannheim, Indianapolis, IN). The reaction mixture was incubated for 48 h at 37°C.

(iii) Endoproteinase Lys-C Cleavage. Approximately 2 mg of the purified protein was precipitated with 90% (v/v) ethanol and the pellet resuspended in a total volume of 1.0 ml of PBS containing 0.1% TX-100. This preparation was added directly to a vial containing 15 μ g of endoproteinase Lys-C (Boehringer Mannheim). The reaction mixture was incubated for 48 h at 37°C.

(iv) Separation of Peptides. The above cleavage reaction mixtures were centrifuged in an Eppendorf centrifuge at 12,000 rpm for 5 min and the supernatant loaded directly onto a Vydac Protein C4 HPLC column (The Separations Group, Hesperia, CA). The solvents used were 0.1% (v/v) aqueous trifluoroacetic acid (TFA) [Solvent A] and acetonitrile:H₂O:TFA, 80:20:0.1 (v/v/v) [Solvent B] at a flow rate of 1.0 ml/min. Following the initial wash with Solvent A, the peptides were eluted with a linear gradient between 0 and 100% of Solvent B and detected by absorbance at 220 nm. Suitable fractions were collected, dried in a Speed-Vac concentrator (Jouan Inc., Winchester, VA) and resuspended in distilled water. The fractions were separated by SDS-PAGE in 10 to 18% (w/v, acrylamide) gradient gels (ISS) in a Tris-Tricine buffer system (Schägger and von Jagow, 1987). The fractions containing a single peptide band were submitted directly for N-terminal sequence analysis. Fractions displaying multiple peptide bands in SDS-PAGE were electrophoretically transferred onto a PVDF membrane as described above. The membrane was stained with Coomassie Brilliant Blue R-

250 and the individual bands excised before submitting them for N-terminal sequence analysis (Matsudaira, 1987).

Determination of subunit size. Determination of molecular weight by Matrix Assisted Laser Desorption/Ionization-Time of Flight (MALDI-TOF) mass spectrometry (Hillenkamp and Karas, 1990) was done on a Lasermat 2000 Mass Analyzer (Finnigan Mat, Hemel Hempstead, UK) with 3,5-dimethoxy-4-hydroxy-cinnamic acid as the matrix. Cold ethanol precipitation was done on samples containing $\geq 0.1\%$ (v/v) TX-100 to remove the detergent. The final ethanol concentration was 90% (v/v). The precipitated protein was resuspended in water.

Determination of aggregate sizes by gel filtration chromatography. Approximately 1 mg of the purified protein was precipitated with 90% (v/v) ethanol and the pellet resuspended in a total volume of 1.0 ml of PBS containing 0.1% TX-100. Two hundred microliters of the preparation were applied to a Superose-6 HR 10/30 gel filtration column (10 \times 30 mm, Pharmacia) equilibrated in PBS /0.1% TX-100 at a flow rate of 0.5 ml/min. The column was calibrated using the HMW Calibration Kit (Pharmacia) which contains aldolase with a size of 158,000, catalase with a size of 232,000; ferritin with a size of 440,000; thyroglobulin with a size of 669,000; and blue dextran with sizes between 2000 and 2,000,000.

Amino Acid Sequence Analysis. N-terminal sequence analysis was carried out using an Applied Biosystems Model 477A Protein/Peptide Sequencer equipped with an on-line Model 120A PTH Analyzer (Applied Biosystems, Foster City, CA). The phenylthiohydantoin (PTH) derivatives were identified by reversed-phase HPLC using a Brownlee PTH C-18 column (particle size 5 μm , 2.1 mm i.d. \times 22 cm 1.; Applied Biosystems).

Immunizations. Female BALB/c mice (Taconic Farms, Germantown, NY), age 6-8 weeks, were immunized subcutaneously with two doses of UspA1 or UspA2 four weeks apart. To prepare the vaccine, purified UspA1 or UspA2 was added to aluminum phosphate, and the mixture rotated overnight at 4°C. 3-O-deacylated monophosphoryl lipid A (MPL) (Ribi ImmunoChem Research, Inc.) was added just prior to administration. Each dose of vaccine contained 5 μg of purified protein, 100 μg of aluminum phosphate and 50 μg of MPL resuspended in a 200 μl volume. Control mice were injected with 5 μg of CRM₁₉₇ with the same adjuvants. Serum samples were collected before the first vaccination and two weeks after

the second immunization. Mice were housed in a specific-pathogen free facility and provided water and food *ad libitum*.

Monoclonal antibodies. The 17C7 MAb was secreted by a hybridoma (ATCC HB11093). MAbs 13-1, 29-31, 45-2, and 6-3 were prepared as previously described (Chen *et al.*, 1995).

Murine model of *M. catarrhalis* pulmonary clearance. This model was performed as described previously (Chen *et al.*, 1995).

Enzyme linked immunosorbent assay (ELISA) procedures. Two different ELISA procedures were used. One was used to examine the reactivity of sera to whole bacterial cells and the other the reactivity to the purified proteins.

For the whole cell ELISA, the bacteria were grown overnight on Mueller-Hinton agar and swabbed off the plate into PBS. The turbidity of the cells was adjusted to 0.10 at 600 nm and 100 μ l added to the wells of a 96 well Nunc F Immunoplate (Nunc, Roskilde, Denmark). The cells were dried overnight at 37°C, sealed with a mylar plate sealer and stored at 4°C until needed. On the day of the assay, the residual protein binding sites were blocked by adding 5% non-fat dry milk in PBS with 0.1% Tween 20 (Bovine Lacto Transfer Technique Optimizer [BLOTTO]) and incubating 37°C for one hour. The blocking solution was then removed and 100 μ l of sera serially diluted in the wells with blotto. The sera were allowed to incubate for 1 h at 37°C. The plate wells were soaked with 300 ml PBS containing 0.1% Tween 20 for 30 seconds and washed 3 times for 5 seconds with a Skatron plate washer and then incubated 1 hr at 37°C with goat anti-mouse IgG conjugated to alkaline phosphatase (BioSource) diluted 1:1000 in blotto. After washing, the plates were developed at room temperature with 100 μ l per well of 1 mg/ml p-nitrophenyl phosphate dissolved in diethanolamine buffer. Development was stopped by adding 50 μ l of 3N NaOH to each well. The absorbance of each well was read at 405 nm and titers calculated by linear regression. The titer was reported as the inverse of the dilution extrapolated to an absorption value of 0.10 units.

For the ELISA against the purified proteins, the proteins were diluted to a concentration of 5 μ g/ml in a 50 mM sodium carbonate buffer (pH 9.8) containing 0.02% sodium azide (Sigma Chemical Co.). One hundred microliters were added to each well of a 96 well

E.I.A./R.I.A medium binding ELISA plate (Costar Corp., Cambridge, MA) and incubated for 16 hours at 4°C. The plates were washed and subsequently treated the same as described for whole cell ELISA procedure.

Complement-dependent bactericidal assay. For this assay, 20 µl of the bacterial suspension containing approximately 1200 cfu bacteria in PBS supplemented with 0.1 mM CaCl₂, MgCl₂ and 0.1% gelatin (PCMG) were mixed with 20 µl of serum diluted in PCMG and incubated for 30 min at 4°C. Complement, prepared as previously described (Chen *et al.*, 1996), was added to a concentration of 20%, mixed, and incubated 30 min at 35°C. The assay was stopped by diluting with 200 µl of cold, 4°C, PCMG. 50 µl of this suspension was spread onto Mueller-Hinton plates. Relative killing was calculated as the percent reduction in cfu in the sample relative to that in a sample in which heat inactivated complement replaced active complement.

Inhibition of bacterial adherence to HEp-2 cells. The effect of specific antibodies on bacterial adherence to HEp-2 cells was examined. A total of 5×10^4 HEp-2 cells in 300 µl of RPMI-10 were added to a sterile 8-well Lab-Tek chamber slide (Nunc, Inc., Naperville, Ill) and incubated overnight in a 5% CO₂ incubator to obtain a monolayer of cells on the slide. The slide was washed with PBS and incubated with 300 µl of bacterial suspension ($A_{550}=0.5$) or with a bacterial suspension that had been incubated with antisera (1:100) at 37°C for 1 h. The slides were then washed with PBS and stained with the Difco quick stain following the manufacturer's instructions. The slide was viewed and photographed using a light microscope equipped with a camera (Nikon Microphot-SA, Nikon, Tokyo, Japan).

Protein interaction with fibronectin and vitronectin. The interactions of purified UspA1 and UspA2 with fibronectin were examined by dot blot. Human plasma fibronectin (Sigma Chemical Co., St. Louis, MO) was applied to a nitrocellulose membrane, and the membrane blocked with blotto for 1 h at room temperature. The blot was then washed with PBS and incubated with purified UspA1 or UspA2 (2 µg/ml in blotto) overnight at 4°C. After three washes with PBS, the membrane was incubated with the MAb 17C7 diluted in blotto for 2 h at room temperature and then with goat anti-mouse immunoglobulin conjugated to alkaline phosphatase (BIO-RAD Lab. Hercules, Calif.) (1:2,000 in PBS with 5% dry milk, 2 h, room temperature). The membrane was finally developed with a substrate solution containing

nitroblue tetrazolium and 5-bromo-chloro-3-indolyl phosphate in 0.1 M tris-HCl buffer (pH 9.8).

Interaction with vitronectin was examined by a similar procedure. The purified UspA1 and UspA2 were spotted onto the nitrocellulose membrane and the membrane blocked with blotto. The membrane was then incubated sequentially with human plasma vitronectin (GIBCO BRL, Grand Island, N.Y., 1 µg/ml in blotto), rabbit anti-human vitronectin serum (GIBCO BRL), goat anti-rabbit IgG-alkaline phosphatase conjugate and substrate.

Interaction with HEp-2 cells by the purified protein. Each well of a 96 well cell culture plate (Costar Corp., Cambridge, Mass.) was seeded with 5×10^4 HEp-2 cells in 0.2 ml RPMI containing 10% fetal calf serum and the plate incubated overnight in a 37°C incubator containing 5% CO₂. Purified UspA1 or UspA2 (1 to 1,000 ng) in blotto was added and incubated at 37°C for 2 h. The plate was washed with PBS, and incubated with the 1:1 mixed mouse antisera to either UspA1 or UspA2 (1:1000 dilution in PBS containing 5% dry milk), the plate was washed and incubated with rabbit anti-mouse IgG conjugated to horseradish peroxidase (1:5,000 in PBS containing 5% dry milk) (Brookwood Biomedical, Birmingham, AL) at room temperature for 1 h. Finally, the plate was washed and developed with a substrate solution containing 2,2'-azino-bis-(3-ethyl-benzthiazoline-6-sulfonic acid) at 0.3 mg/ml in pH 4.0 citrate buffer containing 0.03% hydrogen peroxide (KPL, Gaithersburg, MD). Whole bacteria of strain O35E were included as a positive control. The highest concentration of the bacteria tested had an optical density of $A_{550}=1.0$. The abscissa for the bacterial data shown in FIG. 7 plots the values for three fold dilutions of the bacterial suspension.

Results

Purification of UspA1 and UspA2. The inventors developed a large-scale, high yield process for extracting and purifying UspA2 from a pellet of *M. catarrhalis* cells. The method consisted of three critical steps. First the UspA2 protein was extracted from the bacteria with pH 8.0, 0.03 M THT. Second, the cell extract was applied to a TMAE column and the UspA2 protein eluted with NaCl. Finally, the enriched fractions from the TMAE chromatography were applied to a ceramic hydroxyapatite column and the UspA2 eluted with a linear NaPO₄ gradient. A yield of 250 mg of purified UspA2 was typically obtained from ~400 g wet weight of *M. catarrhalis* O35E strain cells. A single band was seen for the UspA2 in SDS-PAGE gels

by Coomassie blue staining. It corresponded to a molecular size of ~240,000 and contained greater than 95% of the protein based on scanning densitometry (FIG. 6A). A second band reacting with the 17C7 MAb at approximately 125,000 could be detected in the UspA2 preparation by western but not by Coomassie blue staining (FIG. 6C). The cells need not be
5 lysed to achieve this high yield, which suggested this protein is present in large amounts on the surface of the bacterium.

A method for the purification of the UspA1 protein was also developed. This protein co-purified with UspA2 through the initial extraction and TMAE chromatography steps. Following hydroxyapatite chromatography, however, UspA1 remained bound to the column
10 and had to be eluted at the higher salt concentration of 500 mM NaPO₄. The crude UspA1 preparation obtained in this step was reapplied and eluted from the hydroxyapatite column using a linear sodium phosphate gradient. A total of 80 mg of purified UspA1 was isolated from ~1.6 kg wet wt. of *M. catarrhalis* O35E strain cells. UspA1 purified using this method migrated at three different apparent sizes on SDS-PAGE depending on the method of sample
15 preparation. Unheated samples exhibited a single band at ~280,000, whereas samples heated at 100°C for 3 min resulted in an apparent molecular weight shift to ~350,000. Prolonged heating at 100°C resulted in a shift of the 350,000 band to one at 100,000 (FIG. 6B). Following heating of the sample for 7 min at 100°C, the band at 100,000 contained greater than 95% of the protein based on scanning densitometry of the Coomassie stained gel. In contrast, UspA2 migrated at
20 240,000 regardless of the duration of the heating when examined by SDS-PAGE. The different migration behaviors indicated the preparations contained two distinctly different proteins

Molecular Weight Determinations. MALDI-TOF mass spectrometric analysis for determination of molecular weight of UspA2 using 3,5-dimethoxy-4-hydroxy-cinnamic acid matrix in presence of 70% (v/v) aqueous acetonitrile and 0.1% TFA resulted in the
25 identification of a predominant species with average molecular mass of 59,518 Da. In addition to the expected $[M+H]^+$ and $[M+2H]^{2+}$ molecular ions, the $[2M+H]^+$ and $[3M+H]^+$ ions were also observed. The latter two ions were consistent with the dimer and the trimer species. Using similar conditions, the inventors were unable to determine the mass of UspA1.

To determine the molecular sizes of the purified proteins in solution, UspA1 and UspA2
30 were independently run on a Superose-6 HR 10/30 gel filtration column (optimal separation

range: 5,000-5,000,000) calibrated with molecular weight standards. Purified UspA1 exhibited a native molecular size of 1,150,000 and UspA2 a molecular size of 830,000. These sizes, however, may be affected by the presence of TX-100.

N-terminal Sequence Analysis of Internal UspA1 and UspA2 Peptides. All attempts to determine the N-terminal sequences of both UspA and UspA1 proved unsuccessful. No sequence could be determined. This suggested two things. First, the N-terminus of both proteins were blocked, and, second, neither protein preparation contained contaminating proteins that were not N-terminally blocked.

Thus, to confirm that the primary sequence of purified UspA1 and UspA2 corresponded to that deduced from their respective gene sequences, internal peptide fragments were generated and subjected to N-terminal sequence analysis. Tables X and XI show the N-terminal sequences obtained for fragments generated from the digestion of the UspA2 and UspA1 proteins, respectively. The sequences matching the primary amino acid sequence deduced from the respective gene sequences are indicated for each fragment. The UspA2 fragments #3 and #4 exhibited sequence similarity with residues 505-515 and 605-614 respectively of the amino acid sequence deduced from the UspA1 gene. In Table XII, UspA1 fragment #3 exhibited sequence similarity with residues #278-294 of the UspA2 primary sequence. These sequences corresponded with the domains within UspA1 and UspA2 that share 93% sequence identity. The remainder of the sequences, however, were unique to the respective proteins.

TABLE X

N-terminal sequences of internal UspA2 peptide cleavage fragments

UspA2 Fragment Sequence ^a	Match ^b	Cleavage
1) LLAEQQLNG SEQ ID NO:73	92-100	Trypsin
2) ALESNVEEGL SEQ ID NO:74	216-225	Lys-C
	245-254	
	274-283	
3) ALESNVEEGLLDLS SEQ ID NO:75	274-288	Trypsin
	*505-515	

TABLE X cont'd

UspA2 Fragment Sequence ^a	Match ^b	Cleavage
4) AKASAANTDR SEQ ID NO:76	378-387	Chymotrypsin
	* 605-614	
5) AATAADAITKNGN SEQ ID NO:77	439-450	Chymotrypsin
6) SITDLGTKVDGFDGR SEQ ID NO:78	458-472	Lys-C
7) <u>VD</u> ALXTKVNALDXKVN SEQ ID NO:79	473-488	Trypsin
8) AAQAALSGLF <u>VP</u> YSVGKFNATAALGGYGSK SEQ ID NO:80	506-535	CNBr

^aUnderlined residues denote mismatch with the nucleotide derived amino acid sequence.

Ambiguous residues whose identity could not be verified are denoted by the letter X.

^bAsterisk (*) indicates match with UspA1. Without asterisk indicates matches with nucleotide
5 derived amino acid sequence of UspA2.

TABLE XI

N-terminal sequences of internal UspA1 peptide cleavage fragments

UspA1 Fragment Sequence ^a	Match ^b	Cleavage
1) LENNVEE <u>P</u> XLNLS	456-468	Lys-C
2) DQKADI	473-478	Trypsin
3) NNVEEGLLDLSGRLIDQK	504-521	Lys-C
	* 278-294	
4) VA <u>E</u> GFEIF	690-697	Trypsin
5) AGIATNKQELILQNDRLNRI	701-720	Lys-C

^aAs per Table X. X denotes an unidentified amino acid residue.

^bAsterisk (*) indicates match with UspA2. Without asterisk indicates matches with nucleotide
10 derived amino acid sequence of UspA1.

Reactivity of MAbs with UspA1 and UspA2. The western blot analysis of purified UspA1 and UspA2 revealed that both proteins reacted strongly with the MAb 17C7 described by Helminen *et al.* (1994) (FIG. 7). The reactivity of the proteins with other MAbs was also
15 investigated. The data in Table XII show that, whether assayed by ELISA or western, the

MAbs 13-1, 29-31 and 45-2 only reacted with UspA2, the MAbs 7D7, 29C6, 11A6 and 12D5 only reacted with UspA1, while 17C7 and 6-3 reacted with both UspA1 and UspA2. All the MAbs shown in Table XIII bind to whole bacteria when examined by ELISA. These results indicated that UspA2 was exposed on the surface of the bacterium.

5

TABLE XII

Summary of reactivity of monoclonal antibodies with purified UspA1,
UspA2 and whole bacteria of strain O35E

mAb	Isotype	Reactivity		
		Whole bacterium ^a	Purified UspA1 ^b	Purified UspA2 ^b
13-1	IgG1κ	+	-	+
29-31	IgG1λ	+	-	+
45-2	IgG2a	+	-	+
17C7	IgG2a	+	+	+
6-3	IgM	+	+	+
7D7	IgG2b	+	+	-
29C6	IgG1	+	+	-
11A6	IgA	+	+	-
12D5	IgG1	+	+	-

^aDetermined by whole cell ELISA.

^bDetermined by ELISA and western blot.

10

TABLE XIII

Cross-reactivity of antibodies to UspA1 and UspA2 proteins

Antiserum to	Geometric mean ELISA titer ^b to	
	UspA1	UspA2
UspA1 ^a	740,642 ^c	10,748 ^c
UspA2 ^a	19,120 ^d	37,615 ^d

^aThe preparation of the sera are described in the text.

^bELISA titers are for total IgG and IgM antibodies for sera pooled from ten mice.

^cThe difference in titer of the anti-UspA1 with the two purified proteins was statistically different by the Wilcoxon signed rank test ($p=0.0002$).

^dThe difference in titer of the anti-UspA2 with the two purified proteins was statistically different by the Wilcoxon signed rank test ($p=0.01$).

Immunogenicity and antibody cross-reactivity. Antisera to the purified UspA1 and UspA2 proteins were generated in mice. The titers of antigen specific antibodies (IgG and IgM) as well as the cross-reactive antibodies in these sera were determined by an ELISA assay using each of the purified proteins (Table XIII). Both proteins elicited antibody titers that were greater against themselves than against the heterologous protein. Thus, the reactivities of both the MAbs (Table XII) as well as the polyclonal antibodies indicate that the proteins possessed both shared and non-shared B-cell epitopes.

Antibody reactivity to whole bacterial cells and bactericidal activity. Antisera to the UspA1 and UspA2 were assayed by whole cell ELISA against the homologous O35E strain and several heterologous isolates (Table XIV). The antibodies to UspA1 and to UspA2 reacted strongest with the O35E strain. The reactivity of the sera toward the heterologous isolates indicated they bound antibodies elicited by both UspA1 and UspA2.

TABLE XIV

ELISA and complement mediated bactericidal titers toward whole bacterial cells of multiple isolates of *M. catarrhalis* elicited by purified UspA1 and purified UspA2

Isolate	<u>Whole cell ELISA^a</u>		<u>Bactericidal titer^b</u>	
	anti-UspA1 ^a	anti-UspA2 ^a	anti-UspA1	anti-UspA2
O35E	195,261	133,492	400	800
430-345	12,693	18,217	400	400
1230-359	7,873	13,772	400	400
TTA24	14,341	7,770	800	800

^aTiter determined for pool of sera from ten mice. The titer of the sera drawn before the first immunization was less than 50 for all isolates.

^bBactericidal titers were determined as the inverse of the highest serum dilution killing greater than 50% of the bacteria. The titers for the sera from mice immunized contemporaneously with CRM₁₉₇ were less than 100.

The bactericidal activities of the antisera to UspA1 and UspA2 were determined against O35E and other isolates as well (Table XIV). Both sera had bactericidal titers ranging from 400-800 against O35E and the disease isolates. Anti-CRM₁₉₇ serum, the negative control, as well as sera drawn before immunization, had a titers of <100 against all the strains. These results were consistent with the previous observation that the epitopes shared by the two proteins are highly conserved among isolates and the antibodies toward those isolates are bactericidal.

Pulmonary challenge. Immunized mice were given a pulmonary challenge with the homologous O35E strain or the heterologous TTA24 strain. Relative to the control mice immunized with CRM₁₉₇, enhanced clearance of both strains was observed regardless of whether the mice were immunized with UspA1 or UspA2 (Table XV). No statistical difference ($p > 0.05$) was seen between the groups of mice immunized with UspA1 and with UspA2.

TABLE XV
Pulmonary clearance of *M. catarrhalis* by mice immunized with
purified UspA1 and UspA2

Study	Immunogen	Challenge strain	% clearance ^a	p ^a
1	UspA1	O35E	49.0	0.013
	UspA2		31.8	0.05
	CRM ₁₉₇		0	-
2	UspA1	TTA24	54.6	0.02
	UspA2		66.6	0.0003
	CRM ₁₉₇		0	-

^aChallenge method described in text. Numbers are the percentage of bacteria cleared from the immunized mice compared to control mice which were immunized with CRM₁₉₇.

Interaction of purified proteins with HEp-2 cells. The purified UspA1 and UspA2 were tested for their ability to interact with HEp-2 cell monolayer in a 96-well plate using an ELISA. Protein binding to the HEp-2 cells was detected with a 1:1 mix of the mouse antisera to UspA1 and UspA2. Purified UspA1 bound to HEp-2 cells at concentrations above 10 ng. A weak binding by the UspA2 was detected at concentrations above 100 ng (FIG. 7). The attachment of O35E bacteria to HEp-2 cells was used as a positive control. This result, plus the data showing that the anti-UspA1 antibodies inhibited attachment of the bacteria to HEp2 cells, suggests UspA1 plays an important role in bacterial attachment which also suggested that UspA1 was exposed on the bacterial surface.

Interaction of purified proteins with fibronectin and vitronectin. The purified proteins were assayed for their ability to interact with fibronectin and vitronectin by dot blot assays. Human plasma fibronectin immobilized on a nitrocellulose membrane bound purified UspA1 but not UspA2 (FIG. 8), while UspA2 immobilized on the nitrocellulose membrane was capable of binding vitronectin (FIG. 8). Vitronectin binding by the UspA1 was also detected, but the reactivity was weaker. Collagen (type IV), porcine mucin (type III), fetuin and heparin were also tested for interaction with purified UspA1 and purified UspA2, but these did not exhibit detectable binding.

Discussion

Previous UspA purification attempts yielded preparations containing multiple high molecular weight protein bands by SDS-PAGE and western blot. Because each of the bands reacted with the "UspA specific" MAb 17C7, it was thought they represented multiple forms of the UspA protein (Chen *et al.*, 1996). However, the inventors have discovered that there are two distinct proteins, UspA1 and UspA2, that share an epitope recognized by the 17C7 MAb. These two proteins are encoded by different genes. This study shows that UspA1 and UspA2 can be separated from one another. The isolated proteins had different SDS-PAGE mobility characteristics, different reactivity with a set of monoclonal antibodies, and different internal peptide sequences. The results, however, were consistent with the proteins sharing a portion of their peptide sequences, including the MAb 17C7 epitope. The separation of the proteins from one another has allowed the inventors to further demonstrate how the proteins were different as well as examine their biochemical, functional, and immunological characteristics.

In solution, the purified proteins appear to be homopolymers of their respective subunits held together by strong non-covalent forces. This is indicated by the fact that UspA2 lacks any cysteines and treatment of both proteins with reducing agents did not alter their mobilities in SDS-PAGE. Both gene sequences possess leucine zipper motifs that might mediate coil-coil interactions (O'Shea *et al.*, 1991). Even so, it was surprising that the non-covalent bonds of both proteins were not only strong enough to resist dissociation by the conditions normally used to prepare samples for SDS-PAGE, but also high concentrations of chaotropic agents such as urea (Klingman and Murphy, 1994) and guanidine HCl. Of the two proteins, UspA2 appeared to be less tightly aggregated, this was indicated by the fact that its subunit size of 59,500 Da could be determined by mass spectrometry. UspA1, however, was recalcitrant to dissociation by all the methods tried, and this may be the reason its size could not be determined by mass spectrometry. In SDS-PAGE, the dominant UspA2 migrated with an apparent size of 240,000 while a far smaller portion migrated at about 125,000 and could only be detected by western analysis. The mobility of UspA1, however, varied depending on how long the sample was heated. The smallest form was about 100,000. This was consistent with the size of the gene product missing from the *uspA1* mutant but not with the size predicted from the gene sequence of 88,000 Da. In solution, both proteins formed larger aggregates than those seen by SDS-PAGE. Their sizes, as measured by gel filtration chromatography, were 1,150,000 and 830,000

for UspA1 and UspA2 respectively. If the proteins behave this way *in vivo*, UspA1 and UspA2 likely occur as large molecular complexes on the bacterial surface of the bacterium.

The results of the N-terminal amino acid sequence analyses of the UspA2 and UspA1 derived peptides (Tables X and XI) were in agreement with the protein sequences derived from the respective gene sequences. This confirmed that the purified UspA1 and UspA2 proteins were the products of the respective *uspA1* and *uspA2* genes. Further, the experimental and theoretical amino acid compositions of UspA1 and UspA2 were consistent, given the size of the proteins and the accuracy of the amino acid determination. There was, however, a discrepancy between the size determined by mass spectrometry of 59,518 and the size indicated from the gene sequence for UspA2 of 62,483. This discrepancy suggested that this protein either undergoes post-translational processing or proteolytic degradation.

The data also suggest that both proteins are exposed on the bacterial surface. That at least one of the proteins is exposed is evident from the finding that the MAb 17C7 and polyclonal sera react with whole cells. The reactivities of the UspA2 specific monoclonal antibodies 13-1, 29-31 and 45-2 with the bacterial cells in the whole cell ELISA provided evidence that the UspA2 is a surface protein (Table XII). The reactivities of the UspA1 specific MAbs 7D7, 29C6, 11A6 and 12D5 with the bacterial cells in the whole cell ELISA provided evidence that the UspA1 is a surface protein (Table XII). Further evidence for surface exposure of UspA1 was indicated by the inhibitory effect of the antiserum on bacterial attachment to HEP-2 cells. The sera to the UspA2 lacked this activity. Thus, both UspA1 and UspA2 appeared to be surface exposed on the bacterium.

Surface exposure of the proteins is probably important for the two proteins' functions. One function for UspA1 appears to be mediation of adherence to host tissues. The evidence for this was that UspA1 antibodies inhibited bacterial binding to HEP-2 cells and the purified protein itself bound to the cells. The relevance of binding to HEP-2 cells is that they are epithelial cells derived from the larynx, a common site of *M. catarrhalis* colonization (Schalen *et al.*, 1992). This confirms the inventors findings that mutants that do not express UspA1 fail to bind epithelial cells. The inventors' also showed that UspA1 binds fibronectin. Fibronectin has been reported to be a host receptor for other pathogens (Ljungh and Wadström, 1995; Westerlund and Korhonen, 1993). Examination of the gene sequence, however, failed to reveal

any similarity with the fibronectin binding motifs reported for Gram positive organisms (Westerlund and Korhonen, 1993). Thus, it is fairly clear that UspA1 plays a role in host adherence, possibly *via* cell associated fibronectin.

5 The function of UspA2 is less certain. Antibodies toward it did not block adherence to the HEP-2 or Chang cell lines, nor did the purified protein bind to those cells. Yet, UspA2 bound vitronectin strongly. Pathogen binding of vitronectin has been linked to host cell adherence (Gomez-Duarte *et al.*, 1997; Limper *et al.*, 1993); however, van Dijk and his co-workers have reported that vitronectin binding by *M. catarrhalis* may be used by the bacteria to subvert host defenses (Verdiun *et al.*, 1994). The soluble form of vitronectin, known as complement factor S, regulates formation of the membrane attack complex (Su, 1996). They suggest that the binding of vitronectin to the *M. catarrhalis* surface inhibits the formation of the membrane attack complex, rendering the bacteria resistant to the complement dependent killing activity of the sera. They have also described two types of human isolates: one that binds vitronectin and is resistant to the lytic activity of the serum and the other that does not bind vitronectin and is serum sensitive (Hol *et al.*, 1993). It must be noted, however, that vitronectin, like all the extracellular matrix proteins, has many forms and serves multiple functions in the host (Preissner, 1991; Seiffert, 1997). Thus, the interaction of both UspA1 and UspA2 with the extracellular matrix proteins fibronectin and vitronectin may serve the bacterium in ways beyond subverting host defenses or as receptors for bacterial adhesion.

20 Even though the two proteins share epitopes and sequences, they have different biochemical activities and likely serve different biological functions. If an immune response to the respective protein interferes with its function, it ought to be considered as a vaccine candidate. The results of the immunological studies in mice indicated that both proteins would be good vaccine candidates. Mice immunized with either UspA1 or UspA2 developed high antibody titers toward the homologous and heterologous bacterial isolates. Further, the sera from these mice had complement dependent bactericidal activity toward all the isolates tested. In addition, immunized mice exhibited enhanced pulmonary clearance of the homologous isolate and heterologous isolates. It is important to note that antibodies elicited by the proteins were partially cross-reactive. This was expected since both react with the 17C7 MAb and share amino acid sequence.

**EXAMPLE V: The Level and Bactericidal Capacity of Child and Adult Human
Antibodies Directed against the Proteins UspA1 and UspA2**

To determine if humans have naturally acquired antibodies to the UspA1 and UspA2 of
5 the *M. catarrhalis* and the biological activity of these antibodies if present, sera from healthy
humans of various ages was examined using both ELISA and a bactericidal assay. It was found
that healthy people have naturally acquired antibodies to both UspA1 and UspA2 in their sera,
and the level of these antibodies and their bactericidal capacity were age-dependent. These
10 results also indicate that naturally acquired antibodies to UspA1 and UspA2 are biologically
functional, and thus support their use as vaccine candidates to prevent *M. catarrhalis* disease.

Material and methods

Bacteria. The *M. catarrhalis* strains O35E and TTA24 were as described in Example I.
An ATCC strain (ATCC 25238) and three other clinical isolates from the inventors' collection
15 were also used.

Human sera. Fifty-eight serum samples were collected from a group of ten children at 2,
4, 6, 7, 15 and 18 months of age who had received routine childhood immunizations.
Individual sera from twenty-six adults and fifteen additional children 18-36 months of age were
also assayed. All sera were obtained from clinically healthy individuals. Information on *M.*
20 *catarrhalis* colonization and infection of these subjects was not collected. The sera were stored
at -70°C.

Purification of UspA1 and UspA2. Purified UspA1 and UspA2 were made from the
O35E strain of *M. catarrhalis* as described in Example IV herein. Each protein preparation
contained greater than 95% of the specific protein based on densitometric scanning of
25 Coomassie brilliant blue stained SDS-PAGE. Based on western blot analysis using monoclonal
antibodies, each purified protein contained no detectable contamination of the other.

Purification of UspA1 and UspA2 specific antibodies from human plasma. Human
plasmas from two healthy adults were obtained from the American Red Cross (Rochester, N.Y.)
and pooled. The antibodies were precipitated by adding ammonium sulfate to 50% saturation.
30 The precipitate was collected by centrifugation and dialyzed against PBS. A nitrocellulose

membrane (2 × 3 inches) was incubated with UspA1 or UspA2 at 0.5 mg/ml in PBS containing 0.1% (vol/vol) Triton X-100 for 1 h at room temperature, washed twice with PBS and residual binding sites on the membrane blocked with 5% (wt/vol) dry milk in PBS for 2 h at room temperature. The membrane was then sequentially washed twice with PBS, 100 mM glycine (pH 2.5) and finally with PBS before incubation with the dialyzed antibody preparation. After incubating for 4 h at 4°C, the membrane was washed again with PBS, and then 10 mM Tris buffer (pH 8.0) containing 1 M sodium chloride to remove non-specific proteins. The bound antibodies were eluted by incubation in 5 ml of 100 mM glycine (pH 2.5) for 2 min with shaking. One ml of Tris-HCl (1M, pH 8.0) was immediately added to the eluate to neutralize the pH. The eluted antibodies were dialyzed against PBS and stored at -20°C.

Enzyme-linked immunosorbent assay (ELISA). Antibody titers to the O35E and other *M. catarrhalis* strains were determined by a whole-cell ELISA as previously described using biotin-labeled rabbit anti-human IgG or IgA antibodies (Brookwood Biomedical, Birmingham, Alabama) (Chen *et al.*, 1996). Antibody titers to UspA1 and UspA2 were determined by a similar method except that the plates were coated with 0.1 µg of purified protein in 100 µg of PBS per well overnight at room temperature. The IgG subclass antibodies to UspA1 or UspA2 were determined using sheep anti-human IgG subclass antibodies conjugated to alkaline phosphatase (The Binding Site Ltd., San Diego, Calif.). The antibody end point titer was defined as the highest serum dilution giving an A₄₁₅ greater than three times that of the control. The control wells received all treatments except human sera and usually had absorbance values ranging from 0.03 to 0.06.

The specificity of biotin-labeled rabbit anti-human IgG and IgA antibodies was determined against purified human IgG, IgM and IgA (Pierce, Rockford, IL) by ELISA. No cross-reactivity was found. The assay sensitivity determined by testing against purified human antibodies of appropriate isotype in an ELISA was 15 and 60 ng/ml in the IgG and IgA assays, respectively. Likewise, the specificity of the human IgG subclass antibody assays was confirmed in ELISA against purified human myeloma IgG subclass proteins (ICN Biomedicals, Inc., Irvine, CA), and the assay sensitivity was 15 ng/ml in the IgG1, IgG3 and IgG4 assays, and 120 ng/ml in the IgG2 assay. Two control sera were included to control for assay to assay variation.

Complement dependent bactericidal assay. The bactericidal activity of the human sera was determined as described previously (Chen *et al.*, 1996). In some studies, the sera were absorbed with purified UspA1 or UspA2 prior to the assay. The absorption of specific antibodies from these sera was accomplished by adding the purified proteins to 20 or 50 µg/ml final concentration. The final serum dilution was 1:10. The mixtures were incubated for 2 h at 4°C and the precipitate removed by micro-centrifugation. The purified human antibodies specific for UspA1 and UspA2 were assayed against five *M. catarrhalis* strains in a similar manner.

Statistics. Statistical analysis was performed on logarithmic transformed titers using JMP software (SAS institute, Cary, N.C.). To allow transformation, a value of one half the lowest serum dilution was assigned to sera which contained no detectable titers. Comparison of IgG levels among the age groups was done by analysis of variance, and the relationship of antibody titer and the bactericidal titer was determined by logistic regression. A *p* value less than 0.05 was considered significant.

Results

Comparison of serum IgG and IgA titers to UspA1 and UspA2 in children and adults.

The IgG and IgA antibody titers in the sera from ten children collected longitudinally between 2-18 months of age, as well as the random samples from fifteen 18-36 month old children and twenty-six adults were determined against the whole bacterial cells of the O35E strain, the purified UspA1 and the purified UspA2 by ELISA. IgG titers to all three antigens were detected in almost all the sera (FIG. 9). The IgG titers to UspA1 and UspA2 exhibited strong age-dependent variation when compared to IgG titers to the O35E bacterium (FIG. 9). The adult sera had significantly higher IgG titers to the purified proteins than sera from children of various age groups ($p < 0.01$). Sera from children at 6-7 months of age had the lowest IgG titers to UspA proteins and the mean titer at this age was significantly lower than that at 2 months of age ($p < 0.05$).

The level of IgA antibodies to UspA1, UspA2 and O35E bacterial cells were age dependent (FIG. 9). A serum IgA titer against the UspA1 and UspA2 was detected in all twenty-six adults and children of 18-36 months of age. For children less than 18 months of age, the proportion exhibiting antigen specific IgA titers increased with age. The mean IgA titers to

UspA1, UspA2 or O35E bacterium in these sera were low for the first 7 months of age but gradually increased thereafter (FIG. 9).

Age-dependent subclass distribution of IgG antibodies to UspA1 and UspA2. The IgG subclass titers to the UspA1 and UspA2 antigens were determined on sera from ten adult sera and thirty-five children's sera. The subclass distribution was found to be age-dependent. The most prominent antibodies to the UspA1 and UspA2 antigens were of the IgG1 and IgG3 subclasses, which were detected in almost all sera. The IgG2 and IgG4 titers were either undetectable or extremely low. Therefore, only data on IgG1 and IgG3 subclasses are reported (FIG. 10). The IgG3 titers against UspA1 or UspA2 in the adult sera were significantly higher than the IgG1 titers ($p < 0.05$). The same subclass profile was seen in the sera from the 2 month old children, although the difference between IgG1 and IgG3 titers did not reach statistical significance, probably because of the smaller sample size. Sera from children between 4 and 36 months of age all had a similar subclass profile which was different from that of the adults and 2 month old children. The IgG1 titers in children's sera were either higher than or equivalent to the IgG3 titers. The mean IgG1 titer to either UspA1 or UspA2 was significantly higher than IgG3 titer to the same antigens in these children's sera ($p < 0.05$).

Bactericidal activity. The bactericidal titers of seventeen sera representing different age groups were determined (Table XVI). All the adult sera and three out of five sera from the two month old children which had high IgG titers to the UspA proteins had strong bactericidal activity. Sera from 6 month old children had the least bactericidal activity. All five sera from this age group had a marginal bactericidal titer of 50, the lowest dilution assayed. The bactericidal activity of the sera from 18 to 36 month old children was highly variable with titers ranging from less than 50 to 500. There was a significant linear relationship between the bactericidal titers and the IgG antibody titers against both UspA1 and UspA2 by logistic regression analysis ($p < 0.01$) (FIG. 11).

TABLE XVI

The level of IgG antibodies to UspA1 and UspA2 from normal human serum
and the serum bactericidal activity

Subject ^a	Age	ELISA IgG titer ^b		BC titer ^c
		UspA1	UspA2	
1	2 month	17,127	6,268	500
	6 month	4,273	1,363	50
	15 month	798	250	<50
2	2 month	12,078	12,244	500
	6 month	1,357	878	50
	18 month	14,041	14,488	200
3	2 month	30,283	20,362	500
	6 month	1,077	1,947	50
	18 month	2,478	1,475	<50
4	2 month	2,086	869	<50
	6 month	530	802	50
	18 month	9,767	8,591	200
5	2 month	3,233	2,655	<50
	6 month	2,246	360	50
	18 month	26,693	43,703	500
6	1.5-3 year	4,036	2,686	50
7	1.5-3 year	2,037	1,251	50
8	1.5-3 year	341	251	<50
9	1.5-3 year	2,538	1,200	500
10	1.5-3 year	1078	1,370	500
11	1.5-3 year	1,265	953	50

TABLE XVI (Continued)

Subject ^a	Age	ELISA IgG titer ^b		BC titer ^c
		UspA1	UspA2	
12	adult	161,750	87,180	450
13	adult	873,680	248,290	>1350
14	adult	154,650	146,900	450
15	adult	10,330	7,860	50
16	adult	35,780	31,230	150
17	adult	19,130	132,200	450

^aThree consecutive samples from subjects 1 through 5 were collected at the stated ages.

^bELISA end point titers to purified UspA1 or UspA2 from the O35E strain were determined as the highest serum dilution giving an A₄₁₅ greater than three times the background.

^cBC titers: bactericidal titer assayed against the O35E strain. Sera were assayed at 1:50, 100, 200, and 500. Bactericidal titer was determined as the highest serum dilution resulting in killing of 50% or more of the bacteria relative to the control. Control bacteria were incubated with test serum and heat inactivated complement serum.

Bactericidal activity of sera absorbed with purified UspA1 or UspA2. Because normal human sera contain antibodies to numerous antigens of *M. catarrhalis* as indicated by western blot, an absorption method was used to determine the contribution of UspA1 and UspA2 specific antibodies towards the bactericidal activity. Six adult sera were absorbed with purified UspA1 or UspA2, and the change in ELISA reactivity to UspA proteins determined. A reduction in ELISA reactivity was seen for all the sera after absorption (Table XVII). Further, absorption with one protein resulted in a reduction of IgG titers to the other protein. Reduction of UspA2 reactivity was of the same degree regardless of whether the absorbent was UspA1 or UspA2. In contrast, there was less reduction in UspA1 reactivity after absorption with UspA2 than with UspA1 (Table XVII). This indicated that antibodies to UspA1 and UspA2 were partially cross-reactive.

TABLE XVII
ELISA titer of adult sera before and after absorption^a

Absorbent	IgG titers to UspA1 in sample ^b					
	#1	#2	#3	#4	#5	#6
saline	161,750	873,680	154,650	10,330	35,780	19,130
UspA1	2,450	2,210	3,160	1,650	<500	3,010
UspA2	42,620	90,150	33,570	6,420	3,490	4,130
	IgG titers to UspA2 ^b					
	#1	#2	#3	#4	#5	#6
saline	87,180	248,290	146,900	7,860	31,230	13,200
UspA1	2,800	2,120	2,700	2,220	<500	<500
UspA2	<500	1,820	3,010	2,960	<500	<500

^aAbsorption: An aliquot of adult serum was diluted and added with purified UspA1 or UspA2 from O35E strain to a final 50 µg/ml protein concentration and final 1:10 serum dilution. The mixtures were incubated at 4°C for 2 h, and precipitates removed by microcentrifugation.

^bIgG titers against the UspA1 and UspA2 proteins were end point titers determined with a starting serum dilution of 1:500.

The bactericidal titers of the absorbed sera were determined and compared with those seen before absorption (Table XVIII). Absorption with either UspA1 or UspA2 resulted in complete loss of bactericidal activity (<50) for all six sera when assayed against the O35E strain, the strain from which the purified proteins were made (Table XVIII). The bactericidal activity of the absorbed sera was also reduced by at least three fold when assayed against the heterologous strain 1230-359. Absorption using UspA1 resulted in greater reduction of the bactericidal titer against the heterologous strain in 3 out of 6 samples compared to absorptions using UspA2 (Table XVIII). This result was consistent with the difference in the reductions of ELISA titers to the UspA1 after absorption with the two proteins. Absorption using the combined proteins UspA1 and UspA2 did not result in further reduction of the bactericidal activity compared to UspA1 alone. All six human sera contained antibodies to a 74 kDa OMP from *M. catarrhalis* as determined by western blot analysis, and absorption using the purified 74 kDa protein did not affect the bactericidal activity of either the O35E strain or the 1230-357

strain. This indicated that antibodies to the UspA proteins were the major source of the bactericidal activity against *M. catarrhalis* in adult sera.

TABLE XVIII

Bactericidal titer of the adult human sera before and after absorption^a

Adsorbent	Bactericidal titer to O35E strain in sample ^b					
	#1	#2	#3	#4	#5	#6
saline	450	>1350	450	50	150	450
UspA1	<50	<50	<50	<50	<50	<50
UspA2	<50	150	<50	<50	<50	<50
	Bactericidal titer to 1230-359 strain ^b					
	#1	#2	#3	#4	#5	#6
saline	450	4050	>1350	150	150	450
UspA1	50	150	<50	<50	50	150
UspA2	150	1350	450	<50	50	50

^aSera were the same as those described in Table XVII.

^bBactericidal titer: The bactericidal activity was measured against the O35E or 1230-359 strains with 3-fold diluted sera starting at 1:50. The highest serum dilution resulting in 50% or greater killing was determined as the bactericidal titer. The purified UspA1 and UspA2 proteins used for absorption were made from the O35E strain.

Because only small volumes of the children sera were available, absorption of these sera was done using a mixture of UspA1 and UspA2 proteins. Absorption resulted in the complete loss or a significant reduction of bactericidal activity in four out of seven sera (Table XIX). The four sera including three from two month old children all had an initial bactericidal titer of 200 or greater prior to absorption. The other three sera, which did not show a change in bactericidal titer upon absorption, all had a marginal titer of 50 before absorption. The reduction in ELISA reactivity to the UspA proteins after absorption confirmed that the antibody concentration had been reduced. This suggested that antibodies specific for the UspA1 and UspA2 proteins in children's sera were also a major source of the bactericidal activity towards *M. catarrhalis*.

TABLE XIX
Bactericidal activity of children's sera before and after absorption with
pooled purified UspA1 and UspA2^a

Sample	Age (months)	Unabsorbed serum		Absorbed serum	
		A ₄₁₅ ^b	BC titer ^c	A ₄₁₅ ^b	BC titer ^c
1	2	0.84	200	0.29	<50
2	2	0.93	200	0.19	<50
3	2	0.98	500	0.38	50
4	18	0.88	200	0.43	50
5	15	0.66	50	0.25	50
6	18	0.62	50	0.32	50
7	15	0.68	50	0.35	50

^aAbsorption: Each serum was absorbed with a mixture of UspA1 and UspA2 proteins from O35E strain at final protein concentrations of 200, 50 or 20 µg/ml. The same result was seen for all three absorptions of each sample. Only the data from the assay using 20 µg/ml of protein are shown.

^bA₄₁₅: The absorbance at 415 nm in ELISA using the mixture of UspA1 and UspA2 as detection antigen. Sera were tested at a 1:300 dilution.

^cBC titer: Highest serum dilution resulting in 50% or greater killing of the O35E strain in the assay. Sera were assayed at dilutions 1:50, 200, and 500.

Affinity purified antibodies to UspA1 and UspA2: To confirm their cross-reactivity and bactericidal activity, antibodies to UspA1 or UspA2 from adult plasma were isolated by an affinity purification procedure. The purified antibodies reacted specifically with the UspA1 and the UspA2 proteins but not with non-UspA proteins in the O35E lysates in a western blot assay. The purified antibodies to one protein also reacted to the other with almost equivalent titer in ELISA (Table XX). Both antibody preparations exhibited reactivity with five *M. catarrhalis* strains in the whole-cell ELISA and bactericidal assay (Table XXI). The bactericidal titers against all five *M. catarrhalis* strains ranged between 400 and 800, which was equivalent to 0.25-0.50 µg/ml of the protein in the purified antibody preparations (Table XXI).

TABLE XX

Cross-reactivity of affinity purified human antibodies to UspA1 and UspA2 in
ELISA

Antibodies purified to ^a	IgG titers against ^b	
	UspA1	UspA2
UspA1	50,468	20,088
UspA2	53,106	52,834

^aThe antibodies were purified from plasma pooled from two healthy adults by immune elution using purified UspA1 or UspA2 from the O35E strain immobilized on nitrocellulose membrane.

^bELISA end point titers are the highest antibody dilutions giving an A_{415} greater than three times the background.

TABLE XXI

Whole cell ELISA titer and bactericidal titer of affinity purified human
antibodies to UspA1 and UspA2^a

Assay strain	Whole cell ELISA titer ^b		BC titer ^c	
	Ab to UspA1	Ab to UspA2	Ab to UspA1	Ab to UspA2
O35E	12,553	9,939	400	800
ATCC25238	30,843	29,512	400	400
TTA24	51,511	57,045	800	800
216:96	31,140	23,109	400	400
1230-359	8,495	16,458	800	800

^aThe purified antibody preparations were the same as described in Table XX. The specific reactivities of the purified antibodies to UspA proteins, but not other outer membrane proteins, were confirmed by western blots.

^bELISA end point titers are the highest antibody dilutions giving an A_{415} greater than three times the background when assayed against whole bacterial cells.

^cBC titer: Highest antibody dilution resulting in 50% or greater killing of the bacterial inoculum in the assay. Antibodies (120 μ g/ml) were assayed at dilutions 1:100, 200, 400, and 800.

Discussion

Previous studies examining human antibodies to *M. catarrhalis* whole cells or outer membrane proteins usually focused on a single age group. Further, the biological function of the antibodies was left largely undetermined (Chapman *et al.*, 1985), and the antigens eliciting the functional antibodies were not identified. Thus, these previous studies did not provide information as to the role of naturally acquired antibodies in protection against *M. catarrhalis* diseases, nor did they provide clear information as to what antigens are suitable for vaccine development. The data from this study indicate that the IgG antibodies to UspA1 and UspA2 are present in normal human sera and their levels are age-dependent. These antibodies are an important source of serum bactericidal activity in both children and adults.

These data indicated that most children had serum IgG antibodies to both UspA1 and UspA2 at two months of age although the level varied from individual to individual, and the IgG subclass profile in these infant sera was similar to that in adult sera. The infant sera had bactericidal activity. The absorption studies suggested that the bulk of the bactericidal antibodies in these sera were directed against the UspA1 and the UspA2 proteins. These results suggest that the IgG antibodies detected in the two month old children are of maternal origin. This is consistent with the report that umbilical cord serum contains high titers of antibodies to an extract of *M. catarrhalis* whole cells (Ejlertsen *et al.*, 1994b).

Due to the lack of clinical information on the study subjects and small number of subjects examined in this study, it could not be determined whether maternal antibodies against UspA, although bactericidal *in vitro*, were protective in young children. However, at two months of age the children had significantly higher serum IgG titers against the UspA proteins and only a few of these children had a low level of IgA antibodies to *M. catarrhalis* as compared to children at 15-18 months of age. If serum IgA reflects prior mucosal exposure to the bacterium, then most of the children are not infected by *M. catarrhalis* in the first few months of age. One of the reasons may be that the maternal antibodies present in the young children protect them from infection at this age. This is consistent with the finding that young children seldom carry this bacterium and do not develop *M. catarrhalis* disease during the first months of life (Ejlertsen *et al.*, 1994a).

Children may become susceptible to *M. catarrhalis* infection as maternal antibodies wane. In this study, the sera from 6 to 7 month old children had the lowest level of IgG antibodies to the UspA proteins and barely detectable bactericidal titers against whole cells of *M. catarrhalis*. By 15 months of age, nearly all children had serum IgA antibodies to the UspA proteins, and the level of IgA antibodies had significantly increased along with the level of IgG antibodies and bactericidal activity when compared with children of 6 to 7 months of age. This suggested that these children had been exposed to the bacterium and mounted an antibody response. The fifteen sera from the group of 18-36 month old children all had IgG and IgA titers to the UspA proteins and the bactericidal titers varied greatly. The UspA specific IgG antibodies in the older children's sera had different characteristics than the antibodies from the two month old children. First, the IgG1 antibody titer was significantly higher than the IgG3 titer in children's sera, while the opposite was true for the 2 month old children (FIG. 10). Second, most sera from 2 month old children had bactericidal activity, while bactericidal activity was barely detectable in the sera from children of 6 months or older. The low antibody level and the low serum bactericidal activity seen in children between 6-36 months of age is consistent with the epidemiological findings that children of this age group have the highest colonization rate and highest incidence of *M. catarrhalis* disease (Bluestone, 1986; Ejlertsen *et al.*, 1994b; Leinonen *et al.*, 1981; Roitt *et al.*, 1985; Ruuskanen and Heikkinen, 1994; Sethi *et al.*, 1995; Teele *et al.*, 1989).

Adults, a population usually resistant to *M. catarrhalis* infections (Catlin, 1990; Ejlertsen *et al.*, 1994a), were found to have consistently higher levels of IgG antibodies to the UspA proteins as well as higher serum bactericidal activity than children. The bactericidal activity of the adult sera was clearly antibody-mediated since immunoglobulin depleted sera had no activity (Chen *et al.*, 1996), and the antibodies purified from adult plasma exhibited complement dependent bactericidal activity. The antibodies purified from human sera using UspA1 or UspA2 from a single isolate exhibited killing against multiple strains. This result indicates that humans developed bactericidal antibodies toward the conserved epitopes of UspA proteins in response to natural infections.

In all adult samples, the IgG antibodies were primarily of the IgG1 and IgG3 subclasses with IgG3 being higher. This is consistent with previous reports that the IgG3 subclass is a major constituent of the immune response to *M. catarrhalis* in adults and children greater than 4

years of age, but not in younger children (Carson *et al.*, 1994; Goldblatt *et al.*, 1990). Of the four IgG subclasses in humans, IgG3 constitutes only a minor component of the total immunoglobulin in serum. However, IgG3 antibody has the highest affinity to interact with C1q, the initial step in the classic complement pathway leading to elimination of the bacterium by both complement-dependent killing and opsono-phagocytosis (Roitt *et al.*, 1985). Since IgG3 antibody is efficiently transferred across the placenta, it may also confer protective immunity to infants. The data from this study indicate that IgG3 antibody to the UspA proteins is an important component of the immune response to natural infection and has *in vitro* biological activity.

As clinical information related to *M. catarrhalis* infection was not collected for the study subjects, it is unknown how the antibodies to UspA1 or UspA2 were induced. When antibodies made against the UspA proteins in guinea pigs were tested for reactivity with other bacterial species, including *Pseudomonas aeruginosa*, *Neisseria meningitidis*, *Neisseria gonorrhoeae*, *Bordetella pertussis*, *Escherichia coli*, and nontypable *Haemophilus influenzae* by western blot, no reactivity was detected. This suggests that the antibodies were elicited as a specific response to the UspA antigens of *M. catarrhalis*. This is consistent with the high colonization rate and the endemic nature of this organism in human populations. Since the affinity purified antibodies to the two UspA proteins were cross-reactive, it could not be determined whether the human antibodies were elicited by one or both proteins. It seemed clear that the shared sequence between these two proteins was the main target of the bactericidal antibodies.

In summary, this study demonstrated that antibodies to the two UspA proteins are present in nearly all humans regardless of age. The overall level and subclass distribution of these antibodies, however, were age-dependent. IgG antibodies against UspA1 and UspA2 were cross-reactive, and are a major source of serum bactericidal activity in adults. The level of these antibodies and serum bactericidal activity appears to correlate with age-dependent resistance to *M. catarrhalis* infection. Since humans make an antibody response to many other *M. catarrhalis* antigens in addition to UspA1 and UspA2 after natural infection, it remains to be determined if immunization with one or both UspA proteins will confer adequate protection in susceptible populations.

EXAMPLE VI: UspA2 as a Carrier for OligosaccharidesUspA2 as a pneumococcal saccharide carrier.

This study demonstrates that UspA2 can serve as a carrier for a pneumococcal saccharide. A seven valent pneumococcal polysaccharide was conjugated to UspA2 by reductive amination. Swiss Webster mice were immunized on wk 0 and wk 4 and a final bleed taken on wk 6. Each mouse was immunized subcutaneously (s.c.) in the abdomen with 1 µg carbohydrate per dose with aluminum phosphate as the adjuvant. A group of mice was immunized with the PP7F- CRM conjugate as a control. The data for the sera from the 6 wk bleed are shown in Table XXII, Table XXIII, and Table XXIV. The conjugate elicited antibodies against both the polysaccharide as well as bactericidal antibodies to *M. catarrhalis*. These results demonstrate that UspA2 can serve a carrier for eliciting antibodies to this pneumococcal saccharide and retain its immunogenicity to UspA2.

TABLE XXII**Titers elicited by 7F conjugates to the pneumococcal polysaccharide 7F**

Antigen	IgG ELISA titer to Pn Ps 7F*
PP7F-UspA2 mix	<100
PP7F-UspA2 conjugate	9,514
PP7F-CRM conjugate	61,333

*Pool of sera from five mice.

TABLE XXIII**ELISA titers of sera against whole cells of three *M. catarrhalis* isolates**

Immunogen Group ¹	Strain Tested		
	035E	430-345	1230-359
PP7F-UspA2 ² mix	51,409	4,407	9,124
PP7F CRM conjugate	56	49	47
PP7F UspA2 conjugate	31,111	3,529	8,310

¹Vaccine group consists of 5 Swiss-Webster mice. Each group immunized at wk 0 and wk 3 and serum collected at wk 6.

²Vaccine composed of 1 µg Pneumo Type 7F and 1 µg UspA2 adjuvanted with aluminum phosphate.

TABLE XXIV

5 Complement dependent bactericidal antibodies against three *M. catarrhalis* isolates

Immunogen Group ¹	Strain Tested		
	035E	430- 345	1230- 359
PP7F- UspA2 mix	400	400	400
PP7F CRM conjugate	<100	<100	<100
PP7F UspA2 conjugate	400	400	200

¹BC₅₀ titer is highest serum dilution at which >50% of bacteria were killed as compared to serum from wk 0 mice. The most concentrated serum tested was a 1:100 dilution.

UspA2 as an *Haemophilus* b Oligosaccharide Carrier.

10 This study demonstrates that UspA2 can serve as a carrier for an *Haemophilus influenzae* type b oligosaccharide (HbO). An HbO sample (average DP=24) was conjugated to UspA2 by aqueous reductive amination in the presence of 0.1% Triton X-100. The ratio of the HbO to UspA2 was 2:1 by weight. Conjugation was allowed to proceed for 3 days at 35°C and the conjugate diafiltered using an Amicon 100K cutoff membrane. The conjugate ratio (mg carbohydrate/mg UspA2) was 0.43:1. The carbohydrate was determined by orcinol assay and
15 the protein by Lowry. The number of hydroxy-ethyl lysines was determined by amino acid analysis and found to be 12.6.

20 The immunogenicity of the conjugate was examined by immunizing Swiss-Webster mice. The mice were immunized twice on wk 0 and wk 4 with 1 µg of carbohydrate. No adjuvant was used with the conjugate, but was used with UspA2. The sera were pooled and titered. The reactivity toward HbPS by the radioantigen binding assay (RABA) was similar to that seen when HbO is conjugated to CRM₁₉₇ (Table XXV). The whole cell titer toward the homologous *M. catarrhalis* isolate (O35E) was similar to that seen for non-conjugated UspA2
25 (Table XXVI), as were the bactericidal titers (Table XXVII). Thus, when a carbohydrate

antigen that typically elicits a RABA titer less than 0.10 is conjugated to UspA2, it becomes immunogenic.

TABLE XXV

Comparison of immunogenicity of HbO conjugated to UspA2 to HbO conjugated to CRM₁₉₇ to *Haemophilus b* polysaccharide by Radioantigen Binding Assay (RABA)

Week	HbO-CRM ₁₉₇	Hbo-UspA2
0	<0.10	<0.10
3	2.51	2.87
4	4.46	3.56
6	58.66	18.92

TABLE XXVI

Comparison of immunogenicity of HbO-UspA2 conjugate with non-conjugated UspA2 by ELISA against whole cell of the O35E isolate to *M. catarrhalis*

Week	UspA2 ^a	Hbo-UspA2
0	<50	<50
4	54,284	17,424
6	345,057	561,513

^a5 µg UspA2 adjuvanted with 500 µg aluminum phosphate.

TABLE XXVII

Bactericidal of sera toward two *M. catarrhalis* isolates.

Isolate	UspA2 ^a	Hbo-UspA2
O35E	4,500	>4,500
345	n.d.	450

^a5 µg UspA2 adjuvanted with 500 µg aluminum phosphate.

n.d. = not determined

**EXAMPLE VII: Association of mouse serum sensitivity with expression
of mutant forms of UspA2**

When bacteria are killed in the presence of serum that lack specific antibodies toward them, it is called "serum sensitivity." In the case of *M. catarrhalis*, the mutants lacking an intact UspA2 protein have been found to be serum sensitive. These mutants were constructed so that one (O35E.1; refer to Example IX for a description of isolates O35E.1, O35E.2 and O35E.12) did not express UspA1, one (O35E.2) did not express UspA2, and one (O35E.12) did not express either protein based on a lack of reactivity with the 17C7 monoclonal antibody. The O35E.2 and O35E.12, however, expressed a smaller truncated form UspA2 (tUspA2) that reacts with antibodies prepared by immunizing mice with purified UspA2. The tUspA2 could be detected in a western blot of bacterial lysates using either polyclonal anti-UspA2 sera or the MAb 13-1. The size of the smaller form was consistent with the gene truncation used for the construction of the two mutants.

This bactericidal capacity was tested by mixing the non-immune mouse sera, a 1:5 dilution of human complement and a suspension of bacteria (Approx. 1000 cfu) in the wells of a microtiter plate. The mouse sera were tested at both a 1:50 and 1:100 dilution. The number of surviving bacteria was then determined by spreading a dilution of this bacterial suspension on agar growth medium. The killing was considered significant when fewer than 50% viable bacteria as cfu's were recovered relative to the samples without mouse sera. Killing by the non-immune sera was seen only for the mutants lacking a "complete" UspA2 (Table XXVIII).

TABLE XXVIII

Bactericidal activity of the pre- immune sera from Balb/c mice

Mutant	Proteins Expressed	Bactericidal Activity of Normal Mouse Sera
O35E	UspA1 & UspA2	-
O35E.1	UspA2	-
O35E.2	UspA1 & tUspA2	+
O35E.12	tUspA2	+

**EXAMPLE VIII: Identification of a Decapeptide Epitope in
UspA1 that Binds MAb 17C7**

It was clear from the work with different strains of *M. catarrhalis* and analyses of their protein sequences of UspA1 that certain epitopic regions must exist which are similar, if not identical, in all of the strains and provide the basis of the immunogenic response in humans. In order to identify such immunogenic epitope(s), peptides spanning the UspA1 region known to contain the binding site for MAb 17C7 were prepared and examined for their ability to bind to MAb 17C7.

Specifically, overlapping synthetic decapeptides, as shown in Table XXIX and FIG. 12, that were N-terminally bound to a membrane composed of derivatized cellulose were obtained from Research Genetics Inc. (Huntsville, AL). After five washes with PBS-Tween containing 5% (w/v) non-fat dry milk, the membrane was subsequently incubated with MAb 17C7 (in the form of hybridoma culture supernatant) overnight at 4°C. Following three washes with PBS-Tween, the membrane was incubated overnight at 4°C with gentle rocking with 10^6 cpm of radioiodinated (specific activity 2×10^7 cpm/ μ g protein), affinity-purified goat anti-mouse immunoglobulin. The membrane was then washed as before and exposed to X-ray film (Fuji RX safety film, Fuji Industries, Tokyo, Japan).

TABLE XXIX

Decapeptides Used to Identify Binding Site for MAb 17C7

PEPTIDE #	PEPTIDE SEQUENCE	
9	SGRLLDQKAD	SEQ ID NO:81
10	QKADIDNNIN	SEQ ID NO:82
11	NNINNIYELA	SEQ ID NO:83
12	NNIYELAQQQ	SEQ ID NO:84
13	YELAQQQDQH	SEQ ID NO:18
14	AQQQDQHSSD	SEQ ID NO:85
15	QDQHSSDIKT	SEQ ID NO:86
16	HSSDIKTLKN	SEQ ID NO:87
17	DIKTLKNNVE	SEQ ID NO:88
18	TLKNNVEEGL	SEQ ID NO:89
19	EEGLLDLSGR	SEQ ID NO:90
20	LSGRLIDQKA	SEQ ID NO:91
21	DQKADIAKNQ	SEQ ID NO:92
22	AKNQADIAQN	SEQ ID NO:93
23	IAQNQTDIQD	SEQ ID NO:94
24	DIQDLAAYNE	SEQ ID NO:95

It is clear from the dot blot results shown in the autoradiograph (FIG. 13) that peptide 13, YELAQQQDQH (SEQ ID NO:18) exhibited optimal binding of MAb 17C7 with peptide 14 (SEQ ID NO:85) exhibiting less than optimal binding. This same peptide (SEQ ID NO:18) is present in UspA2 which explains why both proteins bind to MAb 17C7.

Interestingly, peptide 12 shows no binding and binding by peptides 15, 16, 19, 22, 23 is probably non-specific. Thus, a comparison of peptides 12, 13, and 14 yields the conclusion that the 7-mer AQQQDQH (SEQ ID NO:17) is an essential epitope for MAb 17C7 to bind to UspA1 and UspA2. This conclusion is in agreement with the current understanding that an immunogenic epitope may comprise as few as five, six or seven amino acid residues.

**Example IX: Phenotypic Effect of Isogenic *uspA1* and *uspA2* Mutations on
M. catarrhalis Strain O35E**

Materials and Methods

Bacterial strains, plasmids and growth conditions. The bacterial strains and plasmids used in this study are listed in Table XXX. *M. catarrhalis* strains were routinely grown at 37°C on Brain-Heart Infusion (BHI) agar plates (Difco Laboratories, Detroit, MI) in an atmosphere of 95% air-5% CO₂ supplemented, when necessary, with kanamycin (20 µg/ml) (Sigma Chemicals Co., St. Louis, MO) or chloramphenicol (0.5 µg/ml) (Sigma), or in BHI broth. The BHI broth used to grow *M. catarrhalis* cells for attachment assays was sterilized by filtration. *Escherichia coli* strains were cultured on Luria-Bertani (LB) agar plates (Maniatis *et al.*, 1982) supplemented, when necessary, with ampicillin (100 µg/ml), kanamycin (30 µg/ml), or chloramphenicol (30 µg/ml).

TABLE XXX

Bacterial Strains and Plasmids Used in this Study

Strain or plasmid	Description	Source or reference
<u><i>M. catarrhalis</i></u>		
O35E	Wild-type isolate from middle ear fluid	Helminen <i>et al.</i> , 1994
O35E.1	Isogenic mutant of O35E with a kan cartridge in the <i>uspA1</i> structural gene	Aebi <i>et al.</i> , 1997
O35E.2	Isogenic mutant of O35E with a kan cartridge in the <i>uspA2</i> structural gene	Aebi <i>et al.</i> , 1997

TABLE XXX (Continued)

Strain or plasmid	Description	Source or reference
O35E.12	Isogenic mutant of O35E with a kan cartridge in the <i>uspA2</i> structural gene and a cat cartridge in the <i>uspA1</i> structural gene	This study
P-44	Wild-type isolate that exhibits rapid hemagglutination	Soto-Hernandez <i>et al.</i> , 1989
P-48	Wild-type isolate that exhibits slow hemagglutination	Soto-Hernandez <i>et al.</i> , 1989
<u><i>Escherichia coli</i></u>		
DH5 α	Host for cloning studies	Stratagene
<u>Plasmids</u>		
pBluescript II	Cloning vector; Amp ^r	Stratagene
pUSPA1	pBluescript II SK+ with a 2.7 kb insert containing most of the <i>uspA1</i> gene of <i>M. catarrhalis</i> strain O35E	Aebi <i>et al.</i> , 1997
pUSPA1CAT	pUSPA1 with a cat cartridge replacing the 0.6 kb <i>Bgl</i> II fragment of the <i>uspA1</i> gene	This study

Characterization of outer membrane proteins. Whole cell lysates and outer membrane vesicles of *M. catarrhalis* strains were prepared as described (Murphy and Loeb, 1989; Patrick *et al.*, 1987). Proteins present in these preparations were resolved by SDS-PAGE and detected

by staining with Coomassie blue or by western blot analysis as described (Helminen *et al.*, 1993a).

Monoclonal antibodies (MAbs). MAb 17C7, a murine IgG antibody that reacts with a conserved epitope of both UspA1 and UspA2 from *M. catarrhalis* strain O35E, as described in earlier examples herein, was used for immunologic detection of these proteins. MAb 17C7 was used in the form of hybridoma culture supernatant fluid in western blot analysis and in the indirect antibody-accessibility assay. MAb 3F12, an IgG MAb specific for the major outer membrane protein of *Haemophilus ducreyi* (Klesney-Tait *et al.*, 1997), was used as a negative control in the indirect antibody-accessibility assay.

Molecular cloning methods. Chromosomal DNA of *M. catarrhalis* strain O35E was used as the template in a polymerase chain reaction (PCR™) system together with oligonucleotide primers derived from either just after the start of the strain O35E *uspA1* open reading frame (*i.e.*, P1 in FIG. 14) or just after the end of this open reading frame (*i.e.*, P2 in FIG. 14). These primers were designed to contain a *Bam*HI restriction site at their 5'-end. The sequence of these primers was:

P1 - 5'-CGGGATCCGTGAAGAAAAATGCCGCAGGT-3' (SEQ ID NO:96);

P2 - 5'-CGGGATCCCGTCGCAAGCCGATTG-3' (SEQ ID NO:97).

DNA fragments were amplified using a PTC 100 Programmable Thermal Controller (MJ Research, Inc., Cambridge, MA) and the GeneAmp PCR™ kit (Roche Molecular Systems, Inc., Branchburg, NJ). PCR™ products were extracted from 0.7% agarose gel slices using the Qiaex Gel Extraction Kit (Qiagen, Inc., Chadsforth, CA) and digested with *Bam*HI (New England Biolabs, Inc., Beverly, MA) for subsequent ligation into the *Bam*HI site of pBluescript II SK+ (Stratagene, La Jolla, CA). Ligation reactions were performed with overnight incubation at 16°C using T4 DNA ligase (Gibco BRL, Inc., Gaithersburg, MD). Competent *E. coli* DH5α cells were transformed with the ligation reaction mixture according to a standard heat-shock procedure (Sambrook *et al.*, 1989) and the desired recombinants were selected by culturing in the presence of an appropriate antimicrobial compound. The 1.3 kb chloramphenicol (*cat*) resistance cartridge was prepared by excision (using *Bam*HI) from pUCΔECAT (Wyeth-Lederle, Rochester, NY). The *cat* cartridge was subsequently ligated into *Bgl*II restriction sites located in the mid-portion of cloned segment from the *uspA1* gene and, after transformation of

competent *E. coli* DH5 cells, recombinant clones were identified by selection on solidified media containing chloramphenicol.

Transformation of *M. catarrhalis*. The electroporation method used for transformation of *M. catarrhalis* strain O35E has been described in detail (Helminen *et al.*, 1993b). Briefly, a 30-ml portion of a logarithmic-phase broth culture (10^9 colony forming units [cfu]/ml) was harvested by centrifugation, washed three times with 10% (v/v) glycerol in distilled water, and resuspended in 100 μ l of the same solution. A 20- μ l portion of these cells was electroporated with 5 μ g of linear DNA (*i.e.*, the truncated *uspA1* gene containing the *cat* cartridge) in 5 μ l of water in a microelectroporation chamber (Cel-Porator Electroporation system; Bethesda Research Laboratories, Gaithersburg, MD) by applying a field strength of 16.2 kV over a distance of 0.15 cm. Following electroporation, the cell suspension was transferred to 1 ml of BHI broth and incubated with shaking at 37°C for 90 min. Ten 100- μ l portions were then spread on BHI agar plates containing the appropriate antimicrobial compound.

Southern blot analysis. Chromosomal DNA purified from wild-type and mutant *M. catarrhalis* strains was digested with either *Pvu*II or *Hind*III (New England Biolabs) and Southern blot analysis was performed as described (Sambrook *et al.*, 1989). Double-stranded DNA probes were labeled with 32 P by using the Random Primed DNA Labeling Kit (Boehringer-Mannheim, Indianapolis, IN).

Indirect antibody-accessibility assay. Overnight BHI broth cultures of *M. catarrhalis* strain O35E and its isogenic mutants were diluted in PBS buffer containing 10% (v/v) fetal bovine serum and 0.025% (w/v) sodium azide (PBS-FBS-A) to density of 110 Klett units (ca. 10^9 cfu/ml) as measured with a Klett-Summerson colorimeter (Klett Manufacturing Co., New York, NY). Portions (100 μ l) of this suspension were added to 1 ml of MAb 17C7 or MAb 3F12 culture supernatant. After incubation at 4°C for one hour with gentle agitation, the bacterial cells were washed once and suspended in 1 ml of PBS-FBS-A. Affinity-purified goat anti-mouse immunoglobulin, radiolabeled with 125 I to a specific activity of 10^8 cpm per μ g, was added and the mixture was incubated for one hour at 4°C with gentle agitation. The cells were then washed four times with 1 ml of PBS-FBS-A, suspended in 500 μ l of triple detergent

(Helminen *et al.*, 1993a) and transferred to glass tubes. The radioactivity present in each sample was measured by using a gamma counter.

Autoagglutination and hemagglutination assays. The ability of *M. catarrhalis* strains to autoagglutinate was assessed using bacterial cells grown overnight on a BHI agar plate. These cells were resuspended in PBS to a turbidity of 400 Klett units in a glass tube and subsequently allowed to stand at room temperature for ten minutes at which time the turbidity of this suspension was again determined. Rapid and slow autoagglutination were defined as turbidities of less than and greater than 200 Klett units, respectively, after 10 minutes. The hemagglutination slide assay using heparinized human group O Rh⁺ erythrocytes was performed as previously described (Soto-Hernandez *et al.*, 1989).

Serum bactericidal assay. Complement-sufficient normal adult human serum was prepared by standard methods. Complement inactivation was achieved by heating the serum for 30 min at 56°C. A *M. catarrhalis* broth culture in early logarithmic phase was diluted in Veronal-buffered saline containing 0.10% (w/v) gelatin (GVBS) to a concentration of $1-2 \times 10^5$ cfu/ml, and 20 µl portions were added to 20 µl of native or heat-inactivated normal human serum together with 160 µl of Veronal-buffered saline containing 5 mM MgCl₂ and 1.5 mM CaCl₂. This mixture was incubated at 37°C in a stationary water bath. At time 0 and at 15 and 30 min, 10 µl aliquots were removed, suspended in 75 µl of BHI broth and spread onto prewarmed BHI agar plates.

Adherence assay. A method used to measure adherence of *Haemophilus influenzae* to Chang conjunctival cells *in vitro* (St. Geme III and Falkow, 1990) was adapted for use with *M. catarrhalis*. Briefly, $2-3 \times 10^5$ HEp-2 cells (ATCC CCL 23) or Chang conjunctival cells (ATCC CCL 20.2) were seeded into each well in a 24-well tissue culture plate (Corning-Costar) and incubated for 24 h before use. A 0.3 ml volume from an antibiotic-free overnight culture of *M. catarrhalis* was inoculated into 10 ml of fresh BHI medium lacking antibiotics and this culture was subsequently allowed to grow to a concentration of approximately 5×10^8 cfu/ml (120 Klett units) with shaking in a gyrotory water bath. The culture was harvested by centrifugation at $6,000 \times g$ at 4-8°C for 10 min. The supernatant was discarded and a Pasteur pipet was used to gently resuspend the bacterial cells in 5 ml of pH 7.4 phosphate-buffered

saline (PBS) or PBS containing 0.15% (w/v) gelatin (PBS-G). The bacterial cells were centrifuged again and this final pellet was gently resuspended in 6-8 ml of PBS or PBS-G.

Portions (25 μ l) of this suspension (10^7 CFU) were inoculated into the wells of a 24-well tissue culture plate containing monolayers of HEp-2 or Chang cells. These tissue culture plates were centrifuged for 5 min at $165 \times g$ and then incubated for 30 min at 37°C . Non-adherent bacteria were removed by rinsing the wells gently five times with PBS or PBS-G, and the epithelial cells were then released from the plastic support by adding 200 μ l of PBS containing 0.05% trypsin and 0.02% EDTA. This cell suspension was serially diluted in PBS or PBS-G and spread onto BHI plates to determine the number of viable *M. catarrhalis* present. Adherence was expressed as the percentage of bacteria attached to the human cells relative to the original inoculum added to the well.

Results

Construction of an isogenic *M. catarrhalis* mutant lacking expression of both UspA1 and UspA2. Construction of *M. catarrhalis* mutants lacking the ability to express either UspA1 (mutant strain O35E.1) or UspA2 (mutant strain O35E.2) has been described in previous examples (Aebi *et al.*, 1997). For constructing a double mutant that lacked expression of both UspA1 and UspA2, the 0.6 kb *Bgl*II fragment of pUSPA1 (FIG. 14A) was replaced by a *cat* cassette, yielding the recombinant plasmid pUSPA1CAT. Using the primers P1 and P2, the 3.2 kb insert of pUSPA1CAT was amplified by PCRTM. This PCRTM product was used to electroporate the kanamycin-resistant *uspA2* strain O35E.2 and yielded the chloramphenicol- and kanamycin-resistant transformant O35E.12, a putative *uspA1 uspA2* double mutant.

Southern blot analysis was used to confirm that strains O35E.1, O35E.2, and O35E.12 were isogenic mutants and that allelic exchange had occurred properly, resulting in replacement of the wild-type *uspA1* or *uspA2* gene, or both, with the mutated allele. Chromosomal DNA preparations from the wild-type parent strain O35E, the *uspA1* mutant O35E.1, the *uspA2* mutant O35E.2, and the putative *uspA1 uspA2* mutant strain O35E.12 were digested to completion with *Pvu*II and probed in Southern blot analysis with DNA fragments derived from these two *M. catarrhalis* genes or with the *kan* cartridge. For probing with the *cat* cartridge, chromosomal DNA from strain O35E.12 was digested with *Hind*III.

The *uspA1*-specific DNA probe was obtained by PCRTM-based amplification of *M. catarrhalis* strain O35E chromosomal DNA using the primers P3 and P4 (FIG. 14A). A 500-bp *uspA2*-specific DNA fragment was amplified from O35E chromosomal DNA by PCRTM with the primers P5 and P6 (FIG. 14B). Use of these two gene-specific probes together with the *kan* and *cat* cartridges in Southern blot analysis confirmed that strain O35E.12 was a *uspA1* *uspA2* double mutant.

Characterization of selected proteins expressed by the wild-type and mutant *M. catarrhalis* strains. Proteins present in outer membrane vesicles extracted from the the wild-type and these three mutant strains were resolved by SDS-PAGE and either stained with Coomassie blue (FIG. 15A) or probed with MAb 17C7 in western blot analysis (FIG. 15B). The wild-type parent strain O35E possessed a very high molecular weight band detectable by Coomassie blue staining (FIG. 15A, lane 1, closed arrow) that was also similarly abundant in the *uspA1* mutant O35E.1 (FIG. 15A, lane 2). The *uspA2* mutant O35E.2 (FIG. 15A, lane 3) had a much reduced level of expression of a band in this same region of the gel; this band was not visible at all in the *uspA1* *uspA2* double mutant O35E.12 (FIG. 2, panel A, lane 4).

Western blot analysis revealed that the wild-type strain (FIG. 15B, lane 1) expressed abundant amounts of MAb 17C7-reactive antigen, most of which had a very high molecular weight, in excess of 220,000. The wild-type strain also exhibited discrete antigens with apparent molecular weights of approximately 120,000 and 85,000 which bound this MAb (FIG. 15B, lane 1, open and closed arrows, respectively). The *uspA1* mutant O35E.1 (FIG. 15B, lane 2) lacked expression of the 120 kDa antigen, which was proposed to be the monomeric form of UspA1, but still expressed the 85 kDa antigen. The amount of very high molecular weight MAb 17C7-reactive antigen expressed by this *uspA1* mutant appeared to be equivalent to that expressed by the wild-type strain. The *uspA2* mutant O35E.2 (FIG. 15B, lane 3) expressed the 120 kDa antigen but lacked expression of the 85 kDa antigen which was proposed to be the monomeric form of the UspA2 protein. In contrast to the *uspA1* mutant, the *uspA2* mutant had relatively little very high molecular weight antigen reactive with MAb 17C7. Finally, the *uspA1* *uspA2* double mutant O35E.12 (FIG. 15B, lane 4) expressed no detectable MAb 17C7-reactive antigens.

Binding of MAb 17C7 to whole cells of the wild-type and mutant strains. The indirect antibody-accessibility assay was used to determine whether both *UspA1* and *UspA2* are exposed on the surface of *M. catarrhalis* and accessible to antibody. Whole cells of both the wild-type strain O35E and the *uspA1* mutant O35E.1 bound similar amounts of MAb 17C7 (Table XXXI). This result suggested that *UspA2* is expressed on the surface of *M. catarrhalis*, or at least on the surface of the *uspA1* mutant. The *uspA2* mutant O35E.2 bound substantially less MAb 17C7 than did the wild-type strain, but the level of binding was still at least an order of magnitude greater than that obtained with an irrelevant IgG Mab directed against a *H. ducreyi* outer membrane protein (Table XXXI). As expected from the western blot analysis, the *uspA1 uspA2* double mutant O35E.12 did not bind MAb 17C7 at a level greater than obtained with the negative controls involving the *H. ducreyi*-specific MAb (Table XXXI).

TABLE XXXI

**Binding of MAb 17C7 to the Surface of Wild-Type
and Mutant Strains of *M. catarrhalis***

Strain	Binding ^a of	
	MAb 17C7	MAb 3F12b
O35E (wild-type)	145,583 ^c	4,924
O35E.1 (<i>uspA1</i> mutant)	154,119	4,208
O35E.2 (<i>uspA2</i> mutant)	96,721	4,455
O35E.12 (<i>uspA1 uspA2</i> double mutant)	6,081	3,997

^a Counts per min of ¹²⁵I-labeled goat anti-mouse immunoglobulin bound to MAbs attached to the bacterial cell surface, as determined in the indirect antibody-accessibility assay.

^b MAb 3F12, a murine IgG antibody specific for a *H. ducreyi* outer membrane protein (Klesney-Tait *et al.*, 1997), was included as a negative control.

^c The values represent the mean of two independent studies.

Characterization of the growth, autoagglutination, and hemagglutination properties of the wild-type and mutant strains. The colony morphology of these three mutant strains grown on BHI agar plates did not differ from that of the wild-type strain parent strain. Similarly, the

rate and extent of growth of all four of these strains in BHI broth were very similar if not identical (FIG. 16). In an autoagglutination assay performed as described in above in the Materials and Methods section of this example, all four strains exhibited the same rate of autoagglutination. Finally, there was no detectable difference between the wild-type parent and the three mutants in a hemagglutination assay using human group O erythrocytes (Soto-Hernandez *et al.*, 1989). Control hemagglutination studies were performed using a pair of *M. catarrhalis* isolates (*i.e.*, strains P-44 and P48) previously characterized as having rapid or slow rates, respectively, of hemagglutination (Soto-Hernandez *et al.*, 1989).

Effect of the *uspA1* and *uspA2* mutations on the ability of *M. catarrhalis* to adhere to human cells. Preliminary studies revealed that the wild-type *M. catarrhalis* strain O35E adhered readily to HeLa cells, HEp-2 cells, and Chang conjunctival cells *in vitro*. To determine whether lack of expression of UspA1 or UspA2 affected this adherence ability, the wild-type and the three mutant strains were first used in an attachment assay with Hep-2 cells. In this set of studies, PBS was used as the diluent for washing the HEp-2 cell monolayers and for serial dilution of the trysinized HEp-2 cell monolayer at the completion of the assay. Both the wild-type strain and the *uspA2* mutant O35E.2 exhibited similar levels of attachment to HEp-2 monolayers (Table XXXI). The *uspA1* mutant O35E.1, however, was less able to adhere to these HEp-2 cells; lack of expression of UspA1 reduced the level of attachment by approximately six-fold (Table XXXII). The *uspA1 uspA2* double mutant O35E.12 exhibited a similarly reduced level of attachment (Table XXXII).

TABLE XXXII
Adherence of Wild-Type and Mutant Strains of *M. catarrhalis*
to HEp-2 and Chang Conjunctival Cells *in vitro*

Strain	Adherence ^a to	
	HEp-2 cells ^b	Chang cells ^c
O35E (wild-type)	14.7 ± 4.9	51.4 ± 30.8
O35E.1 (<i>uspA1</i> mutant)	2.4 ± 0.9 (0.006 ^d)	0.8 ± 0.5 (0.002 ^d)
O35E.2 (<i>uspA2</i> mutant)	19.1 ± 7.0 (0.213 ^d)	55.9 ± 16.7 (0.728 ^d)
O35E.12 (<i>uspA1 uspA2</i> double mutant)	2.3 ± 1.8 (0.011 ^d)	0.6 ± 0.2 (0.002 ^d)

^a Adherence is expressed as the percentage of the original inoculum that was adherent to the human epithelial cells at the end of the 30 min incubation period. Each number represents the mean (± S.D.) of two independent studies.

^b PBS was used for washing of the monolayers and for serial dilutions of adherent *M. catarrhalis*.

^c PBS-G was used for washing of the monolayers and for serial dilutions of adherent *M. catarrhalis*.

^d P value when compared to the wild-type strain O35E using the two-tailed Student t-test.

Control studies revealed, however, that *M. catarrhalis* cells did not survive well in the PBS used for washing of the HEp-2 monolayer and serial dilution of the attached *M. catarrhalis* organisms. When 10⁸ CFU of the wild-type and mutant *M. catarrhalis* strains were suspended in PBS, serially diluted, and allowed to stand for 30 min on ice, the viable number of bacteria decreased to 10⁷ CFU. In contrast, when PBS containing 0.15% (w/v) gelatin (PBS-G) was used for this same type of experiment, there was no reduction in the viability of these *M. catarrhalis* strains over the duration of the experiment. When the HEp-2 cell-based attachment studies were repeated using PBS-G for washing the HEp-2 cell monolayer and as the diluent, there was only a three-fold reduction in adherence of the *uspA1* mutant relative to that obtained with the wild-type parent strain. This finding suggested that the original six-fold difference in attachment ability observed between the wild-type and *uspA1* mutant strain may

have been attributable in part to viability problems caused by the use of the PBS wash and diluent.

Subsequent studies using Chang conjunctival cells as the target for bacterial attachment together with a PBS-G wash and diluent revealed a substantial difference in the attachment abilities of the wild-type strain and the *uspA1* mutant (Table XXXII). Whereas the wild-type and *uspA2* mutant exhibited similar levels of attachment to the Chang cells, the extent of attachment of the *uspA1* mutant was nearly two orders of magnitude less than that of the wild-type parent strain. The *uspA1 uspA2* double mutant also exhibited a much reduced level of attachment similar to obtained with the *uspA1* mutant (Table XXXII).

Effect of the *uspA1* and *uspA2* mutations on serum resistance of *M. catarrhalis*. Similar to the majority of disease isolates of *M. catarrhalis* (Hol *et al.*, 1993; 1995; Verduin *et al.*, 1994), the wild-type strain O35E was resistant to killing by normal human serum *in vitro* (Helminen *et al.*, 1993b). To examine the effect of the lack of expression of UspA1 or UspA2 on serum resistance, the wild-type strain and the three mutant strains were tested in a serum bactericidal assay. Both the wild-type strain (FIG. 17, closed diamonds) and the *uspA1* mutant O35E.1 (FIG. 17, closed triangles) were able to grow in the presence of normal human serum, indicating that lack of expression of UspA1 did not adversely affect the ability of strain O35E.1 to resist killing by normal human serum. However, both the *uspA2* mutant O35E.2 (FIG. 17, closed circles) and the *uspA1 uspA2* double mutant O35E.12 (FIG. 17, closed squares), having in common the lack of expression of UspA2, were readily killed by normal human serum. Heat-based inactivation of the complement system present in this normal human serum eliminated the ability of this serum to kill these latter two mutants (FIG. 17, open circles and squares).

All of the compositions and methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the compositions and methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. More specifically,

it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended
5 claims.

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The following references, to the extent that they provide exemplary procedural or other details supplementary to those set forth herein, are specifically incorporated herein by reference.

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between complement-resistant and complement-sensitive *Moraxella (Branhamella)*
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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Board of Regents, The University of Texas
System

(B) STREET: 201 W. 7th Street

(C) CITY: Austin

(D) STATE: Texas

(E) COUNTRY: USA

(F) POSTAL CODE (ZIP): 78701

(ii) TITLE OF INVENTION: UspA1 AND UspA2 ANTIGENS OF MORAXELLA
CATARRHALIS

(iii) NUMBER OF SEQUENCES: 98

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/033,598

(B) FILING DATE: 20-DEC-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Leu Val
1 5 10 15Ala Cys Ser Glu Phe Ala Lys Gly His Thr Lys Lys Ala Val Leu Gly
20 25 30Ser Leu Leu Ile Val Gly Ala Leu Gly Met Ala Thr Thr Ala Ser Ala
35 40 45Gln Ala Thr Asn Ser Lys Gly Thr Gly Ala His Ile Gly Val Asn Asn
50 55 60Asn Asn Glu Ala Pro Gly Ser Tyr Ser Phe Ile Gly Ser Gly Gly Tyr
65 70 75 80Asn Lys Ala Asp Arg Tyr Ser Ala Ile Gly Gly Gly Leu Phe Asn Lys
85 90 95

Ala Thr Asn Glu Tyr Ser Thr Ile Val Gly Gly Gly Tyr Asn Lys Ala
100 105 110

5 Glu Gly Arg Tyr Ser Thr Ile Gly Gly Gly Ser Asn Asn Glu Ala Thr
115 120 125

Asn Glu Tyr Ser Thr Ile Val Gly Gly Asp Asp Asn Lys Ala Thr Gly
130 135 140

10 Arg Tyr Ser Thr Ile Gly Gly Gly Asp Asn Asn Thr Arg Glu Gly Glu
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15 Tyr Ser Thr Val Ala Gly Gly Lys Asn Asn Gln Ala Thr Gly Thr Gly
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Ser Phe Ala Ala Gly Val Glu Asn Gln Ala Asn Ala Glu Asn Ala Val
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Gly Leu Ser Leu Thr Gly Phe Ala Gly Glu Ser Lys Ala Glu Asn Gly
260 265 270

35 Val Val Ser Val Gly Ser Glu Gly Gly Glu Arg Gln Ile Val Asn Val
275 280 285

Gly Ala Gly Gln Ile Ser Asp Thr Ser Thr Asp Ala Val Asn Gly Ser
290 295 300

40 Gln Leu His Ala Leu Ala Thr Val Val Asp Asp Asn Gln Tyr Asp Ile
305 310 315 320

45 Val Asn Asn Arg Ala Asp Ile Leu Asn Asn Gln Asp Asp Ile Lys Asp
325 330 335

Leu Gln Lys Glu Val Lys Gly Leu Asp Asn Glu Val Gly Glu Leu Ser
340 345 350

50 Arg Asp Ile Asn Ser Leu His Asp Val Thr Asp Asn Gln Gln Asp Asp
355 360 365

Ile Lys Glu Leu Lys Arg Gly Val Lys Glu Leu Asp Asn Glu Val Gly
370 375 380

55 Val Leu Ser Arg Asp Ile Asn Ser Leu His Asp Asp Val Ala Asp Asn
385 390 395 400

Gln Asp Asp Ile Ala Lys Asn Lys Ala Asp Ile Lys Gly Leu Asn Lys
 405 410 415
 5 Glu Val Lys Glu Leu Asp Lys Glu Val Gly Val Leu Ser Arg Asp Ile
 420 425 430
 Gly Ser Leu His Asp Asp Val Ala Thr Asn Gln Ala Asp Ile Ala Lys
 435 440 445
 10 Asn Gln Ala Asp Ile Lys Thr Leu Glu Asn Asn Val Glu Glu Glu Leu
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 15 Leu Asn Leu Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp Ile Asp Asn
 465 470 475 480
 Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
 485 490 495
 20 Ser Asp Ile Lys Thr Leu Lys Asn Asn Val Glu Glu Gly Leu Leu Asp
 500 505 510
 Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln
 515 520 525
 25 Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr
 530 535 540
 30 Asn Glu Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp
 545 550 555 560
 Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn
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 35 Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln
 580 585 590
 Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Val Ser
 595 600 605
 40 Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Glu Ala Asp Ala
 610 615 620
 45 Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Gln Gly
 625 630 635 640
 Glu Ala Leu Val Glu Gln Asn Lys Ala Ile Asn Gln Glu Leu Glu Gly
 645 650 655
 50 Phe Ala Ala His Ala Asp Ile Gln Asp Lys Gln Ile Leu Gln Asn Gln
 660 665 670
 Ala Asp Ile Thr Thr Asn Lys Thr Ala Ile Glu Gln Asn Ile Asn Arg
 675 680 685
 55 Thr Val Ala Asn Gly Phe Glu Ile Glu Lys Asn Lys Ala Gly Ile Ala
 690 695 700

Thr Asn Lys Gln Glu Leu Ile Leu Gln Asn Asp Arg Leu Asn Arg Ile
 705 710 715 720
 5 Asn Glu Thr Asn Asn Arg Gln Asp Gln Lys Ile Asp Gln Leu Gly Tyr
 725 730 735
 Ala Leu Lys Glu Gln Gly Gln His Phe Asn Asn Arg Ile Ser Ala Val
 740 745 750
 10 Glu Arg Gln Thr Ala Gly Gly Ile Ala Asn Ala Ile Ala Ile Ala Thr
 755 760 765
 Leu Pro Ser Pro Ser Arg Ala Gly Glu His His Val Leu Phe Gly Ser
 770 775 780
 Gly Tyr His Asn Gly Gln Ala Ala Val Ser Leu Gly Ala Ala Gly Leu
 785 790 795 800
 20 Ser Asp Thr Gly Lys Ser Thr Tyr Lys Ile Gly Leu Ser Trp Ser Asp
 805 810 815
 Ala Gly Gly Leu Ser Gly Gly Val Gly Gly Ser Tyr Arg Trp Lys
 820 825 830
 25

(2) INFORMATION FOR SEQ ID NO: 2:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATCAGCATGT GAGCAAATGA CTGGCGTAAA TGA CTGATGA GTGTCTATTT AATGAAAGAT 60
 ATCAATATAT AAAAGTTGAC TATAGCGATG CAATACAGTA AAATTTGTTA CGGCTAAACA 120
 40 TAACGACGGT CCAAGATGGC GGATATCGCC ATTTACCAAC CTGATAATCA GTTTGATAGC 180
 CATTAGCGAT GGCATCAAGT TGTGTTGTTG TATTGTCATA TAAACGGTAA ATTTGGTTTG 240
 45 GTGGATGCCC CATCTGATTT ACCGTCCCC TAATAAGTGA GGGGGGGGGG GAGACCCAG 300
 TCATTTATTA GGAGACTAAG ATGAATAAAA TTTATAAAGT GAAGAAAAAT GCCGCAGGTC 360
 ACTTGGTGGC ATGTTCTGAA TTTGCCAAAG GTCATACCAA AAAGGCAGTT TTGGGCAGTT 420
 50 TATTGATTGT TGGGGCGTTG GGCATGGCAA CGACGGCGTC TGCACAAGCA ACCAACAGCA 480
 AAGGCACAGG CGCGCACATC GGTGTTAACA ATAACAACGA AGCCCCAGGC AGTTACTCTT 540
 55 TCATCGGTAG TGGCGGTTAT AACAAAGCCG ACAGATACTC TGCCATCGGT GGTGGCCTTT 600
 TTAACAAAGC CACAAACGAG TACTCTACCA TCGTTGGTGG CGGTTATAAC AAAGCCGAAG 660

	GCAGATACTC	TACCATCGGT	GGTGGCAGTA	ACAACGAAGC	CACAAACGAG	TACTCTACCA	720
	TCGTTGGTGG	CGATGACAAC	AAAGCCACAG	GCAGATACTC	TACCATCGGT	GGTGGCGATA	780
5	ACAACACACG	CGAAGGCGAA	TACTCAACCG	TCGCAGGGGG	CAAGAATAAC	CAAGCCACAG	840
	GTACAGGTTT	ATTTGCCGCA	GGTGTAGAGA	ACCAAGCCAA	TGCCGAAAAC	GCCGTCGCCC	900
10	TGGGTAAAAA	GAACATTATC	GAAGGTGAAA	ACTCAGTAGC	CATCGGCTCT	GAGAATACCG	960
	TTAAAACAGA	ACACAAAAAT	GTCTTTATTC	TTGGCTCTGG	CACAACAGGT	GTAACGAGTA	1020
	ACTCAGTGCT	ACTGGGTAAT	GAGACCGCTG	GCAAACAGGC	GACCACTGTT	AAGAATGCCG	1080
15	AAGTGGGTGG	TCTAAGCCTA	ACAGGATTTG	CAGGGGAGTC	AAAAGCTGAA	AACGGCGTAG	1140
	TTTCTGTGGG	TAGTGAAGGC	GGTGAGCGTC	AAATCGTTAA	TGTTGGTGCA	GGTCAGATCA	1200
20	GTGACACCTC	AACAGATGCT	GTTAATGGCT	CACAGCTACA	TGCTTTGGCC	ACAGTTGTTG	1260
	ATGACAACCA	ATATGACATT	GTTAACAACC	GAGCTGACAT	TCTTAACAAC	CAAGATGATA	1320
	TCAAAGATCT	TCAGAAGGAG	GTGAAAGGTC	TTGATAATGA	GGTGGGTGAA	TTAAGCCGAG	1380
25	ACATTAATTC	ACTTCATGAT	GTTACTGACA	ACCAACAAGA	TGACATCAAA	GAGCTTAAGA	1440
	GGGGGGTAAA	AGAGCTTGAT	AATGAGGTGG	GTGTATTAAG	CCGAGACATT	AATTCAC TTC	1500
30	ATGATGATGT	TGCTGACAAC	CAAGATGACA	TTGCTAAAAA	CAAAGCTGAC	ATCAAAGGTC	1560
	TTAATAAGGA	GGTGAAAGAG	CTTGATAAGG	AGGTGGGTGT	ATTAAGCCGA	GACATTGGTT	1620
	CACTTCATGA	TGATGTTGCC	ACCAACCAAG	CTGACATTGC	TAAAAACCAA	GCGGATATCA	1680
35	AAACACTTGA	AAACAATGTC	GAAGAAGAAT	TATTAAATCT	AAGCGGTCGC	CTGCTTGATC	1740
	AGAAAGCGGA	TATTGATAAT	AACATCAACA	ATATCTATGA	GCTGGCACAA	CAGCAAGATC	1800
40	AGCATAGCTC	TGATATCAAA	ACACTTAAAA	ACAATGTCGA	AGAAGGTTTA	TTGGATCTAA	1860
	GCGGTCGCCT	CATTGATCAA	AAAGCAGATA	TTGCTAAAAA	CCAAGCTGAC	ATTGCTCAAA	1920
	ACCAAACAGA	CATCCAAGAT	CTGGCCGCTT	ACAATGAGCT	ACAAGACCAG	TATGCTCAAA	1980
45	AGCAAACCGA	AGCGATTGAC	GCTCTAAATA	AAGCAAGCTC	TGAGAATACA	CAAAACATTG	2040
	CTAAAAACCA	AGCGGATATT	GCTAATAACA	TCAACAATAT	CTATGAGCTG	GCACAACAGC	2100
50	AAGATCAGCA	TAGCTCTGAT	ATCAAAACCT	TGGCAAAAGT	AAGTGCTGCC	AATACTGATC	2160
	GTATTGCTAA	AAACAAAGCT	GAAGCTGATG	CAAGTTTTGA	AACGCTCACC	AAAAATCAAA	2220
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55	TTGAAGGGTT	TGCGGCTCAT	GCAGATATTC	AAGATAAGCA	AATTTTACAA	AACCAAGCTG	2340

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 25 TCATAACGAT AAATAAATCC ATATCAAATC CAAAATAGCC AATTTGTACC ATGCTAACCA 3120
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 30 CAAAGAATGT TGCCACAACC AAATGCACAC CAAAATTAC CATCACTTGT TTAAACCAA 3300
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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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 Phe Pro Asn Ile Phe Phe Asn Glu Asn His Asp Glu Leu Asp Asp Ala
 35 40 45
 Tyr His Asn Met Ile Leu Gly Asp Thr Ala Ile Val Ser Asn Ser Gln
 50 55 60

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	65					70					75					80	
5	Pro	Asp	Ser	Leu	Leu	Phe	Ser	Lys	Leu	Leu	His	Glu	Gln	Gln	Leu	Asn	
				85					90						95		
	Gly	Phe	Lys	Ala	Gly	Asp	Thr	Ile	Ile	Pro	Leu	Asp	Lys	Asp	Gly	Lys	
				100				105						110			
10	Pro	Val	Tyr	Thr	Lys	Asp	Thr	Arg	Thr	Lys	Asp	Gly	Lys	Val	Glu	Thr	
			115					120					125				
	Val	Tyr	Ser	Val	Thr	Thr	Lys	Ile	Ala	Thr	Gln	Asp	Asp	Val	Glu	Gln	
15				130			135					140					
	Ser	Ala	Tyr	Ser	Arg	Gly	Ile	Gln	Gly	Asp	Ile	Asp	Asp	Leu	Tyr	Asp	
	145					150					155					160	
20	Ile	Asn	Arg	Glu	Val	Asn	Glu	Tyr	Leu	Lys	Ala	Thr	His	Asp	Tyr	Asn	
				165						170					175		
	Glu	Arg	Gln	Thr	Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser	Ser	Ala	
				180					185					190			
25	Asn	Thr	Asp	Arg	Ile	Asp	Thr	Ala	Glu	Glu	Arg	Ile	Asp	Lys	Asn	Glu	
			195					200					205				
	Tyr	Asp	Ile	Lys	Ala	Leu	Glu	Ser	Asn	Val	Glu	Glu	Gly	Leu	Leu	Glu	
30		210					215				220						
	Leu	Ser	Gly	His	Leu	Ile	Asp	Gln	Lys	Ala	Asp	Leu	Thr	Lys	Asp	Ile	
	225				230					235					240		
	Lys	Ala	Leu	Glu	Ser	Asn	Val	Glu	Glu	Gly	Leu	Leu	Glu	Leu	Ser	Gly	
35				245					250						255		
	His	Leu	Ile	Asp	Gln	Lys	Ala	Asp	Leu	Thr	Lys	Asp	Ile	Lys	Ala	Leu	
				260					265					270			
40	Glu	Ser	Asn	Val	Glu	Glu	Gly	Leu	Leu	Asp	Leu	Ser	Gly	Arg	Leu	Leu	
		275						280					285				
	Asp	Gln	Lys	Ala	Asp	Ile	Ala	Lys	Asn	Gln	Ala	Asp	Ile	Ala	Gln	Asn	
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	Gln	Thr	Asp	Ile	Gln	Asp	Leu	Ala	Ala	Tyr	Asn	Glu	Leu	Gln	Asp	Ala	
	305				310					315					320		
	Tyr	Ala	Lys	Gln	Gln	Thr	Glu	Ala	Ile	Asp	Ala	Leu	Asn	Lys	Ala	Ser	
50				325					330					335			
	Ser	Glu	Asn	Thr	Gln	Asn	Ile	Ala	Lys	Asn	Gln	Ala	Asp	Ile	Ala	Asn	
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		355					360					365					

Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg
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 5 Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr
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 Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His Asp Lys Leu
 405 410 415
 10 Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp
 420 425 430
 Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala
 435 440 445
 15 Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp
 450 455 460
 Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Leu
 465 470 475 480
 20 Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser
 485 490 495
 25 Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe
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 Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly
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 30 Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn
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 Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn
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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2596 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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5
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55

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CCACCGATGA TATCATTTAT CTGCTTTTTA GGCATCAGTT ATTTACCGT GATGACTGAT 600
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AAATCGCTGT AACCAGTGCC ATGATTGTTG GCTTGGGTGC GACATCTACT GTGAATGCAC 720
AAGTAGTGGA ACAGTTTTTT CCGAATATCT TTTTAAATGA AAACCATGAT GAATTAGATG 780
ATGCATACCA TAATATGATC TTAGGGGATA CTGCGATTGT ATCTAATTCA CAAGATAATA 840
GTACTCAATT GAAATTTTAT TCTAATGATG AAGATTGAGT TCCTGACAGC CTACTCTTTA 900
GTAACTACT TCATGAGCAG CAACTTAATG GTTTTAAAGC AGGTGACACA ATCATTCTTT 960
TGGATAAGGA TGGCAAACCT GTTTATACAA AGGACACGAG AACAAAGGAT GGTAAAGTAG 1020
AAACAGTTTA TTCGGTCACC ACCAAAATCG CTACCCAAGA TGATGTTGAA CAAAGTGCAT 1080
ATTCACGAGG CATTCAAGGT GATATCGATG ATCTGTATGA CATTAAACCGT GAAGTCAATG 1140
AATACTTAAA AGCAACACAT GATTATAATG AAAGACAAAC TGAAGCAATT GACGCTCTAA 1200
ACAAAGCAAG CTCTGCGAAT ACTGATCGTA TTGATACTGC TGAAGAGCGT ATCGATAAAA 1260
ACGAATATGA CATTAAAGCA CTTGAAAGCA ATGTCGAAGA AGGTTTGTTG GAGCTAAGCG 1320
GTCACCTCAT TGATCAAAAA GCAGATCTTA CAAAAGACAT CAAAGCACTT GAAAGCAATG 1380
TCGAAGAAGG TTTGTTGGAG CTAAGCGGTC ACCTCATTGA TCAAAAAGCA GATCTTACAA 1440
AAGACATCAA AGCACTTGAA AGCAATGTCG AAGAAGGTTT GTTGATCTA AGCGGTCGTC 1500
TGCTTGATCA AAAAGCAGAT ATCGCTAAAA ACCAAGCTGA CATTGCTCAA AACC AAACAG 1560
ACATCCAAGA TCTAGCCGCT TACAACGAGC TACAAGATGC CTATGCCAAA CAGCAAACCG 1620
AAGCGATTGA CGCTCTAAAC AAAGCAAGCT CTGAGAATAC ACAAACATT GCTAAAAACC 1680
AAGCGGATAT TGCTAATAAC ATCAACAATA TCTATGAGCT GGCACAACAG CAAGATCAGC 1740
ATAGCTCTGA TATCAAAACC TTGGCAAAAG CAAGTGCTGC CAATACTGAT CGTATTGCTA 1800
AAAACAAAGC CGATGCTGAT GCAAGTTTTG AAACGCTCAC CAAAATCAA AATACTTTGA 1860
TTGAAAAAGA TAAAGAGCAT GACAAATTAA TTAGTCAAA CAAAACGCG ATTGATGCCA 1920

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ATAAAGCATC TCGGATACC AAGTTTGCAG CGACAGCAGA CGCCATTACC AAAAATGGAA 1980
 ATGCTATCAC TAAAAACGCA AAATCTATCA CTGATTTGGG TACTAAAGTG GATGGTTTTG 2040
 5 ACGGTCGTGT AACTGCATTA GACACCAAAG TCAATGCCTT AGACACCAAA GTCAATGCCT 2100
 TTGATGGTCG TATCACAGCT TTAGACAGTA AAGTTGAAAA CGGTATGGCT GCCCAAGCTG 2160
 10 CCCTAAGTGG TCTATTCCAG CCTTATAGCG TTGGTAAGTT TAATGCGACC GCTGCACTTG 2220
 GTGGCTATGG CTCAAATCT GCGGTTGCTA TCGGTGCTGG CTATCGTGTG AATCCAAATC 2280
 TGGCGTTTAA AGCTGGTGCG GCGATTAATA CCAGTGGTAA TAAAAAAGGC TCTTATAACA 2340
 15 TCGGTGTGAA TTACGAGTTT TAATTGTCTA TCATCACCAA AAAAAAGCAG TCAGTTTACT 2400
 GGCTGCTTTT TTATGGGTTT TTGTGGCTTT TGGTTGTGAG TGATGGATAA AAGCTTATCA 2460
 AGCGATTGAT GAATATCAAT AAATGATTGG TAAATATCAA TAAAGCGGTT TAGGGTTTTT 2520
 20 GGATATCTTT TAATAAGTTT AAAAACCCT GCATAAATA AAGCTGGGCA TCAGAGCTGC 2580
 GAGTAGCGGC ATACAG 2596

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 892 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Leu Val
 1 5 10 15
 Ala Cys Ser Glu Phe Ala Lys Gly His Thr Lys Lys Ala Val Leu Gly
 20 25 30
 Ser Leu Leu Ile Val Gly Ala Leu Gly Met Ala Thr Thr Ala Ser Ala
 35 40 45
 Gln Ala Thr Lys Gly Thr Gly Lys His Val Val Asp Asn Lys Asp Asn
 50 55 60
 Lys Ala Lys Gly Asp Tyr Ser Thr Ala Ser Gly Gly Lys Asp Asn Glu
 65 70 75 80
 Ala Lys Gly Asn Tyr Ser Thr Val Gly Gly Gly Asp Tyr Asn Glu Ala
 85 90 95
 Lys Gly Asn Tyr Ser Thr Val Gly Gly Gly Ser Ser Asn Thr Ala Lys
 100 105 110

Gly Glu Lys Ser Thr Ile Gly Gly Gly Asp Thr Asn Asp Ala Asn Gly
 115 120 125
 Thr Tyr Ser Thr Ile Gly Gly Gly Tyr Tyr Ser Arg Ala Ile Gly Asp
 5 130 135 140
 Ser Ser Thr Ile Gly Gly Gly Tyr Tyr Asn Gln Ala Thr Gly Glu Lys
 145 150 155 160
 Ser Thr Val Ala Gly Gly Arg Asn Asn Gln Ala Thr Gly Asn Asn Ser
 10 165 170 175
 Thr Val Ala Gly Gly Ser Tyr Asn Gln Ala Thr Gly Asn Asn Ser Thr
 15 180 185 190
 Val Ala Gly Gly Ser His Asn Gln Ala Thr Gly Glu Gly Ser Phe Ala
 195 200 205
 Ala Gly Val Glu Asn Lys Ala Asn Ala Asn Asn Ala Val Ala Leu Gly
 20 210 215 220
 Lys Asn Asn Thr Ile Asp Gly Asp Asn Ser Val Ala Ile Gly Ser Asn
 225 230 235 240
 Asn Thr Ile Asp Ser Gly Lys Gln Asn Val Phe Ile Leu Gly Ser Ser
 25 245 250 255
 Thr Asn Thr Thr Asn Ala Gln Ser Gly Ser Val Leu Leu Gly His Asn
 260 265 270
 Thr Ala Gly Lys Lys Ala Thr Ala Val Ser Ser Ala Lys Val Asn Gly
 30 275 280 285
 Leu Thr Leu Gly Asn Phe Ala Gly Ala Ser Lys Thr Gly Asn Gly Thr
 35 290 295 300
 Val Ser Val Gly Ser Glu Asn Asn Glu Arg Gln Ile Val Asn Val Gly
 305 310 315 320
 Ala Gly Asn Ile Ser Ala Asp Ser Thr Asp Ala Val Asn Gly Ser Gln
 40 325 330 335
 Leu Tyr Ala Leu Ala Thr Ala Val Lys Ala Asp Ala Asp Glu Asn Phe
 340 345 350
 Lys Ala Leu Thr Lys Thr Gln Asn Thr Leu Ile Glu Gln Gly Glu Ala
 355 360 365
 Gln Asp Ala Leu Ile Ala Gln Asn Gln Thr Asp Ile Thr Ala Asn Lys
 50 370 375 380
 Thr Ala Ile Glu Arg Asn Phe Asn Arg Thr Val Val Asn Gly Phe Glu
 385 390 395 400
 Ile Glu Lys Asn Lys Ala Gly Ile Ala Lys Asn Gln Ala Asp Ile Gln
 55 405 410 415

Thr Leu Glu Asn Asn Val Gly Glu Glu Leu Leu Asn Leu Ser Gly Arg
 420 425 430

5 Leu Leu Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile Tyr
 435 440 445

Asp Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu
 450 455 460

10 Lys Lys Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile
 465 470 475 480

Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Glu Asn Asn
 485 490 495

15 Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys
 500 505 510

20 Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp
 515 520 525

Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln Tyr Ala Gln
 530 535 540

25 Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Ala Asn
 545 550 555 560

Thr Asp Arg Ile Ala Thr Ala Glu Leu Gly Ile Ala Glu Asn Lys Lys
 565 570 575

30 Asp Ala Gln Ile Ala Lys Ala Gln Ala Asn Glu Asn Lys Asp Gly Ile
 580 585 590

35 Ala Lys Asn Gln Ala Asp Ile Gln Leu His Asp Lys Lys Ile Thr Asn
 595 600 605

Leu Gly Ile Leu His Ser Met Val Ala Arg Ala Val Gly Asn Asn Thr
 610 615 620

40 Gln Gly Val Ala Thr Asn Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp
 625 630 635 640

Ile Ala Asn Asn Ile Lys Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
 645 650 655

45 Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Val Ser Ala Ala Asn
 660 665 670

50 Thr Asp Arg Ile Ala Lys Asn Lys Ala Glu Ala Asp Ala Ser Phe Glu
 675 680 685

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Gln Gly Glu Ala Leu
 690 695 700

55 Val Glu Gln Asn Lys Ala Ile Asn Gln Glu Leu Glu Gly Phe Ala Ala
 705 710 715 720

His Ala Asp Val Gln Asp Lys Gln Ile Leu Gln Asn Gln Ala Asp Ile
 725 730 735
 Thr Thr Asn Lys Ala Ala Ile Glu Gln Asn Ile Asn Arg Thr Val Ala
 740 745 750
 Asn Gly Phe Glu Ile Glu Lys Asn Lys Ala Gly Ile Ala Thr Asn Lys
 755 760 765
 Gln Glu Leu Ile Leu Gln Asn Asp Arg Leu Asn Gln Ile Asn Glu Thr
 770 775 780
 Asn Asn Arg Gln Asp Gln Lys Ile Asp Gln Leu Gly Tyr Ala Leu Lys
 785 790 795 800
 Glu Gln Gly Gln His Phe Asn Asn Arg Ile Ser Ala Val Glu Arg Gln
 805 810 815
 Thr Ala Gly Gly Ile Ala Asn Ala Ile Ala Ile Ala Thr Leu Pro Ser
 820 825 830
 Pro Ser Arg Ala Gly Glu His His Val Leu Phe Gly Ser Gly Tyr His
 835 840 845
 Asn Gly Gln Ala Ala Val Ser Leu Gly Ala Ala Gly Leu Ser Asp Thr
 850 855 860
 Gly Lys Ser Thr Tyr Lys Ile Gly Leu Ser Trp Ser Asp Ala Gly Gly
 865 870 875 880
 Leu Ser Gly Gly Val Gly Gly Ser Tyr Arg Trp Lys
 885 890

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TGTGAGCAAA TGACTGGCGT AAATGACTGA TGAATGTCTA TTTAATGAAA GATATCAATA 60
 TATAAAAGTT GACTATAGCG ATGCAATACA GTAAAATTTG TTACGGCTAA ACATAACGAC 120
 GGTCCAAGAT GCGCGATATC GCCATTTACC AACCTGATAA TCAGTTTGAT AGCCATTAGC 180
 GATGGCATCA AGTTGTGTTG TTGTATTGTC ATATAAACGG TAAATTTGGT TTGGTGGATG 240
 CCCCATCTGA TTTACCGTCC CCCTAATAAG TGAGGGGGGG GGAGACCCCA GTCATTTATT 300
 AGGAGACTAA GATGAACAAA ATTTATAAAG TGAAAAAATA TGCCGCAGGT CACTTGGTGG 360
 CATGTTCTGA ATTTGCCAAA GGCCATACCA AAAAGGCAGT TTTGGGCAGT TTATTGATTG 420

	TTGGGGCATT GGGCATGGCA ACGACGGCGT CTGCACAAGC AACCAAAGGC ACAGGCAAGC	480
5	ACGTTGTTGA CAATAAGGAC AACAAAGCCA AAGGCGATTA CTCTACCGCC AGTGGTGGCA	540
	AGGACAACGA AGCCAAAGGC AATTACTCTA CCGTCGGTGG TGGCGATTAT AACGAAGCCA	600
	AAGGCAATTA CTCTACCGTC GGTGGTGGCT CTAGTAATAC CGCCAAAGGC GAGAAATCAA	660
10	CCATCGGTGG TGGCGATACT AACGACGCCA ACGGCACATA CTCTACCATC GGTGGTGGCT	720
	ATTATAGCCG AGCCATAGGC GATAGCTCTA CCATCGGTGG TGGTTATTAT AACCAAGCCA	780
15	CAGGCGAGAA ATCAACGGTT GCAGGGGGCA GGAATAACCA AGCCACAGGC AACAACTCAA	840
	CGGTTGCAGG CGGCTCTTAT AACCAAGCCA CAGGCAACAA CTCAACGGTT GCAGGTGGCT	900
	CTCATAACCA AGCCACAGGT GAAGGTTTAT TTGCAGCAGG TGTAGAGAAC AAAGCCAATG	960
20	CCAACAACGC CGTCGCTCTA GGTAAAAATA ACACCATCGA TGGCGATAAC TCAGTAGCCA	1020
	TCGGCTCTAA TAATACCATT GACAGTGGCA AACAAAATGT CTTTATTCTT GGCTCTAGCA	1080
25	CAAACACAAC AAATGCACAA AGCGGCTCCG TGCTGCTGGG TCATAATACC GCTGGCAAAA	1140
	AAGCAACCGC TGTTAGCAGT GCCAAAGTGA ACGGCTTAAC CCTAGGAAAT TTTGCAGGTG	1200
	CATCAAAAAC TGGTAATGGT ACTGTATCTG TCGGTAGTGA GAATAATGAG CGTCAAATCG	1260
30	TCAATGTTGG TGCAGGTAAT ATCAGTGCTG ATTCAACAGA TGCTGTTAAT GGCTCACAGC	1320
	TATATGCTTT GGCCACAGCT GTCAAAGCCG ATGCCGATGA AAAC TTAAA GCACTCACCA	1380
35	AAACTCAAAA TACTTTGATT GAGCAAGGTG AAGCACAAGA CGCATTATC GCTCAAAATC	1440
	AAACTGACAT CACTGCCAAT AAAACTGCCA TTGAGCGAAA TTTTAATAGA ACTGTTGTCA	1500
	ATGGGTTTGA GATTGAGAAA AATAAAGCTG GTATTGCTAA AAACCAAGCG GATATCCAAA	1560
40	CGCTTGAAAA CAATGTCGGA GAAGAACTAT TAAATCTAAG CGGTCGCCTG CTTGATCAAA	1620
	AAGCGGATAT TGATAATAAC ATCAACAATA TCTATGATCT GGCACAACAG CAAGATCAGC	1680
45	ATAGCTCTGA TATCAAAACA CTAAAAAAA ATGTCGAAGA AGGTTTGTTG GATCTAAGTG	1740
	GTCGCCTCAT TGATCAAAAA GCAGATCTTA CGAAAGACAT CAAAACACTT GAAAACAATG	1800
	TCGAAGAAGG TTTGTTGGAT CTAAGCGGTC GCCTCATTGA TCAAAAAGCA GATATTGCTA	1860
50	AAAACCAAGC TGACATTGCT CAAAACCAAA CAGACATCCA AGATCTGGCC GCTTACAACG	1920
	AGCTACAAGA CCAGTATGCT CAAAAGCAAA CCGAAGCGAT TGACGCTCTA AATAAAGCAA	1980
55	GCTCTGCCAA TACTGATCGT ATTGCTACTG CTGAATTGGG TATCGCTGAG AACAAAAAAG	2040
	ACGCTCAGAT CGCCAAAGCA CAAGCCAATG AAAATAAAGA CGGCATTGCT AAAAACCAAG	2100

CTGATATCCA GTTGCACGAT AAAAAAATCA CCAATCTAGG TATCCTTCAC AGCATGGTTG 2160
CAAGAGCGGT AGGAAATAAC ACACAAGGTG TTGCTACCAA TAAAGCTGAC ATTGCTAAAA 2220
5 ACCAAGCAGA TATTGCTAAT AACATCAAAA ATATCTATGA GCTGGCACAA CAGCAAGATC 2280
AGCATAGCTC TGATATCAAA ACCTTGGCAA AAGTAAGTGC TGCCAATACT GATCGTATTG 2340
CTAAAAACAA AGCTGAAGCT GATGCAAGTT TTGAAACGCT CACCAAAAAAT CAAAATACTT 2400
10 TGATTGAGCA AGGTGAAGCA TTGGTTGAGC AAAATAAAGC CATCAATCAA GAGCTTGAAG 2460
GGTTTGCGGC TCATGCAGAT GTTCAAGATA AGCAAATTTT ACAAACCAA GCTGATATCA 2520
15 CTACCAATAA GGCCGCTATT GAACAAAATA TCAATAGAAC TGTTGCCAAT GGGTTTGAGA 2580
TTGAGAAAAA TAAAGCTGGT ATTGCTACCA ATAAGCAAGA GCTTATTCTT CAAAATGATC 2640
GATTAAATCA AATTAATGAG ACAAATAATC GTCAGGATCA GAAGATTGAT CAATTAGGTT 2700
20 ATGCACTAAA AGAGCAGGGT CAGCATTTTA ATAATCGTAT TAGTGCTGTT GAGCGTCAAA 2760
CAGCTGGAGG TATTGCAAAT GCTATCGCAA TTGCAACTTT ACCATCGCCC AGTAGAGCAG 2820
25 GTGAGCATCA TGTCTTATTT GGTTTCAGGT ATCACAATGG TCAAGCTGCG GTATCATTGG 2880
GTGCGGCTGG GTTAAGTGAT ACAGGAAAAAT CAACTTATAA GATTGGTCTA AGCTGGTCAG 2940
ATGCAGGTGG ATTATCTGGT GGTGTTGGTG GCAGTTACCG CTGGAAATAG AGCCTAAATT 3000
30 TAACTGCTGT ATCAAAAAAT ATGGTCTGTA TAAACAGACC ATATTTTAT CTAAAAACTT 3060
ATCTTAACTT TTATGAAGCA TCATAAGCCA AAGCTGAGTA ATAATAAGAG ATGTTAAAT 3120
35 AAGAGATGTT AAAACTGCTA AACAATCGGC TTACGACGAT AAAATAAAAT ACCTGGAATG 3180
GACAGCCCCA AAACCAATGC TGAGATGATA AAAATCGCCT CAAAAAATG ACGCATCATA 3240
ACGATAAATA AATCCATATC AAATCCAAAA TAGCCAATTT GTACCATGCT AACCATGGCT 3300
40 TTATAGGCAG CGATTCCCGG CATCATACAA ATCAAGCTAG GTACAATCAA GGCTTTAGGC 3360
GGCAGGCCAT GACGCTGAGC A 3381

45

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 624 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Val Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Ser Val
1 5 10 15

Ala Cys Ser Glu Phe Ala Lys Gly His Thr Lys Lys Ala Val Leu Gly
20 25 30

5 Ser Leu Leu Ile Val Gly Ala Leu Gly Met Ala Thr Thr Ala Ser Ala
35 40 45

Gln Thr Gly Ser Thr Asn Ala Ala Asn Gly Asn Ile Ile Ser Gly Val
50 55 60

10 Gly Ala Tyr Val Gly Gly Gly Val Ile Asn Gln Ala Lys Gly Asn Tyr
65 70 75 80

15 Pro Thr Val Gly Gly Gly Phe Asp Asn Arg Ala Thr Gly Asn Tyr Ser
85 90 95

Val Ile Ser Gly Gly Phe Asp Asn Gln Ala Lys Gly Glu His Ser Thr
100 105 110

20 Ile Ala Gly Gly Glu Ser Asn Gln Ala Thr Gly Arg Asn Ser Thr Val
115 120 125

Ala Gly Gly Ser Asn Asn Gln Ala Val Gly Thr Asn Ser Thr Val Ala
130 135 140

25 Gly Gly Ser Asn Asn Gln Ala Lys Gly Ala Asn Ser Phe Ala Ala Gly
145 150 155 160

30 Val Gly Asn Gln Ala Asn Thr Asp Asn Ala Val Ala Leu Gly Lys Asn
165 170 175

Asn Thr Ile Asn Gly Asn Asn Ser Ala Ala Ile Gly Ser Glu Asn Thr
180 185 190

35 Val Asn Glu Asn Gln Lys Asn Val Phe Ile Leu Gly Ser Asn Thr Thr
195 200 205

Asn Ala Gln Ser Gly Ser Val Leu Leu Gly His Glu Thr Ser Gly Lys
210 215 220

40 Glu Ala Thr Ala Val Ser Arg Ala Arg Val Asn Gly Leu Thr Leu Lys
225 230 235 240

45 Asn Phe Ser Gly Val Ser Lys Ala Asp Asn Gly Thr Val Ser Val Gly
245 250 255

Ser Gln Gly Lys Glu Arg Gln Ile Val His Val Gly Ala Gly Gln Ile
260 265 270

50 Ser Asp Asp Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Tyr Ala Leu
275 280 285

Ala Thr Ala Val Asp Asp Asn Gln Tyr Asp Ile Glu Ile Asn Gln Asp
290 295 300

55 Asn Ile Lys Asp Leu Gln Lys Glu Val Lys Gly Leu Asp Lys Glu Val
305 310 315 320

Gly Val Leu Ser Arg Asp Ile Gly Ser Leu His Asp Asp Val Ala Asp
 325 330 335
 5 Asn Gln Ala Asp Ile Ala Lys Asn Lys Ala Asp Ile Lys Glu Leu Asp
 340 345 350
 Lys Glu Met Asn Val Leu Ser Arg Asp Ile Val Ser Leu Asn Asp Asp
 355 360 365
 10 Val Ala Asp Asn Gln Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Lys
 370 375 380
 Thr Leu Glu Asn Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg
 385 390 395 400
 15 Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn His Ile Tyr
 405 410 415
 20 Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu
 420 425 430
 Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala
 435 440 445
 25 Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu
 450 455 460
 30 Ile Glu Lys Asp Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr
 465 470 475 480
 Ala Ile Asp Ala Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr
 485 490 495
 35 Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys
 500 505 510
 Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val
 515 520 525
 40 Thr Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile Thr Ala
 530 535 540
 Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala Leu Ser
 545 550 555 560
 Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala
 565 570 575
 50 Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala Gly Tyr
 580 585 590
 Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile Asn Thr
 595 600 605
 55 Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr Glu Phe
 610 615 620

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

5 GCCGCACCTG ACCGAGACGC TCCGCCAAAT CAATGCGTCG GTGTACTATG CCCCACCGA 60
15 GCTATGCACG GATAATGGTG CGATGATCGC CTATGCTGGC TTTTGTCTGGC TAAGCCGTGG 120
ACAGTCGGAT GACTTGCGCG TTCGCTGCAT TCCCCGATGG GATATGACAA CGCTTGGTAT 180
20 CGAATATGAT AATTAGGCTG TGGTATTTGA GTTTTGAGTA ATGTACCTAC TACCACTAAT 240
TTATCATACA ATACATAAAC ATAAAAAACA TCGGTATTGT TAAAAAACA TACCCAAGTT 300
AAAATAGCTC AATACTTTAC CATAGCACAA AGAAACTTGT GAACGAAACA TTTAATAATT 360
25 GCCCAAAATG TCACTGCACA CACTTTGTAA AAGCAGGTTT GGGCAATGGC AAACAACGAT 420
ACAAATGCAA AGGTTACCAT CACTATTTTT CTGTGAAGCA ACGAAGCAAC CAAAAAAGTA 480
ATGACATTAA AAAACAAGC CATTGATACA AACAGTAAAC AAATCTTAGG CTTTGTCTGT 540
30 GGTA AACAG ACCTAACAC CTTTAAACGA CTTTATCAGC AGTTAAATAC CCATAACATT 600
CAACTGTTTT TTAGTGACTA CTGGAAATCT TATCGTCAAG TCATTTTAAA GCCAAAACAT 660
35 ATAACAAGCA AAGCTCAAAC TTTTACCATA GAGGACTATA ATAGTCTCAT TGGGCATTTC 720
ATAGCAAGAT TTACAAGAAA GTCAAAGTAT TATTCTAAAT CCGAAAAAAT GATAGAAAAC 780
ACGTTGAATT TATTATTTGC TAAGTGAAT GGTAGCTTAA GATATGTATT TTAATTTAAC 840
40 AATGCCAAAA ACATCAATTA CAGTAAGATT TTAGGCGTTT TGCAGTTGCT ACTTTAGTAA 900
AGCTTTGTTA TACTAGCTGT TAATATACTC AAGCTTGTTT GTGTTTGAGC TATGTTTATT 960
45 TTATAGCAGT AGTTGGTTAT AAAATATAAA TAAAGCTAAG CTCGAGGGTT TGGTAATGGT 1020
TTTTTATGTT TATAATACCA ACAGAGTATC TATACAGCTA AAATAGCTAA TACCTTAGGT 1080
GTATTACAAG TAAAAATCCT TTGTTAATCA GGGAGTGTAT TATATGTATA TTTCCTTTGT 1140
50 ATTTGGTTAT AGCAATCCCT TGGTAAGAAA TCATATCTAT TTTTATTGT TCAATTATTC 1200
AGGAGACTAA GGTGAACAAA ATTTATAAAG TGAAAAAAAT TGCCGCAGGT CATTCCGTGG 1260
55 CATGTTCTGA ATTTGCCAAA GGCCATACCA AAAAGGCAGT TTTGGGCAGT TTATTGATTG 1320
TTGGGGCATT GGGCATGGCA ACGACAGCGT CTGCACAAAC AGGCAGTACA AATGCAGCCA 1380

ACGGCAATAT AATCAGCGGC GTAGGCGCGT ACGTCGGTGG TGGCGTTATA AACCAAGCCA 1440
AAGGCAATTA CCCTACCGTC GGTGGTGGCT TTGATAACCG AGCCACAGGC AATTACTCTG 1500
5 TCATCAGTGG TGGCTTTGAT AACCAAGCCA AAGGCGAGCA CTCTACCATC GCAGGGGGTG 1560
AGAGTAACCA AGCTACAGGT CGTAACTCAA CGGTTGCAGG GGGTTCTAAT AACCAAGCCG 1620
10 TGGGTACAAA CTCAACGGTT GCAGGGGGTT CTAATAACCA AGCCAAAGGT GCAAATTCAT 1680
TTGCAGCAGG TG TAGGTAAC CAAGCCAATA CCGACAACGC CGTCGCTCTA GGTAAAAATA 1740
ACACCATCAA TGGCAATAAC TCAGCAGCCA TCGGCTCTGA GAATACCGTT AACGAAAATC 1800
15 AAAAAAATGT CTTTATTCTT GGCTCTAACA CAACAAATGC ACAAAGCGGC TCAGTACTGC 1860
TAGGTCATGA AACCTCTGGT AAAGAAGCGA CCGCTGTTAG CAGAGCCAGA GTGAACGGCT 1920
20 TAACCCTAAA AAATTTTTCA GGCATATCAA AAGCTGATAA TGGTACTGTA TCTGTCGGTA 1980
GTCAGGGTAA AGAGCGTCAA ATCGTTCATG TTGGTGCAGG TCAGATCAGT GATGATTCAA 2040
CAGATGCTGT TAATGGCTCA CAGCTATATG CTTTGGCTAC AGCTGTTGAT GACAACCAAT 2100
25 ATGACATTGA AATAAACCAA GATAATATCA AAGATCTTCA GAAGGAGGTG AAAGGTCTTG 2160
ATAAGGAAGT GGGTGTATTA AGCCGAGACA TTGGTTCCTT TCATGATGAT GTTGCTGACA 2220
30 ACCAAGCTGA TATTGCTAAA AACAAAGCTG ACATCAAAGA GCTTGATAAG GAGATGAATG 2280
TATTAAGCCG AGACATTGTC TCACTTAATG ATGATGTTGC TGATAACCAA GCTGACATTG 2340
CTAAAAACCA AGCGGATATC AAAACACTTG AAAACAATGT CGAAGAAGGT TTATTGGATC 2400
35 TAAGCGGTCG CCTCATTGAT CAAAAAGCAG ATATTGATAA TAACATCAAC CATATCTATG 2460
AGCTGGCACA ACAGCAAGAT CAGCATAGCT CTGATATCAA AACCTTGGCA AAAGCAAGTG 2520
40 CTGCCAATAC TGATCGTATT GCTAAAAACA AAGCCGATGC TGATGCAAGT TTTGAAACAC 2580
TCACCAAAAA TCAAAATACT TTGATTGAAA AAGATAAAGA GCATGACAAA TTAATTACTG 2640
CAAACAAAAC TGCGATTGAT GCCAATAAAG CATCTGCGGA TACCAAGTTT GCAGCGACAG 2700
45 CAGACGCCAT TACCAAAAAAT GGAAATGCTA TCACTAAAAA CGCAAAATCT ATCACTGATT 2760
TGGGTACTAA AGTGGATGGT TTTGACGGTC GTGTAAGTGC ATTAGACACC AAAGTCAATG 2820
50 CCTTTGATGG TCGCATCACA GCTTTAGACA GTAAAGTTGA AAACGGTATG GCTGCCCAAG 2880
CTGCCCTAAG TGGTCTATTC CAGCCTTATA GCGTTGGTAA GTTTAATGCG ACCGCTGCAC 2940
TTGGTGGCTA TGGCTCAAAA TCTGCGGTTG CTATCGGTGC TGGCTATCGT GTGAATCCAA 3000
55 ATCTGGCGTT TAAAGCTGGT GCGGCGATTA ATACCAGTGG CAATAAAAAA GGCTCTTATA 3060

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ACATCGGTGT GAATTACGAG TTCTAATTGT CTATCATCAC CAAAAAAGC AGTCAGTTTA 3120
 CTGGCTGCTT TTTTATGGGT TTTTATGGCT TTTGGTTGTG AGTGATGGAT AAAAGCTTAT 3180
 5 CAAGCGATTG ATGAATATCA ATAAATGATT GGTAATATC AATAAAGCGG TTAGGGTTT 3240
 TTGGATATCT TTTAATAAGT TAAAAACCC CTGCATAAAA TAAAGCTGGC ATCAG 3295

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Leu Val
 1 5 10 15
 Ala Cys Ser Glu Phe Ala Lys Gly His Thr Lys Lys Ala Val Leu Gly
 20 25 30
 Ser Leu Leu Ile Val Gly Ile Leu Gly Met Ala Thr Thr Ala Ser Ala
 35 40 45
 Gln Met Ala Thr Thr Pro Ser Ala Gln Val Val Lys Thr Asn Asn Lys
 50 55 60
 Lys Asn Gly Thr His Pro Phe Ile Gly Gly Gly Asp Tyr Asn Thr Thr
 65 70 75 80
 Lys Gly Asn Tyr Pro Thr Ile Gly Gly Gly His Phe Asn Thr Ala Glu
 85 90 95
 Gly Asn Tyr Ser Thr Val Gly Gly Gly Phe Thr Asn Glu Ala Ile Gly
 100 105 110
 Lys Asn Ser Thr Val Gly Gly Gly Phe Thr Asn Glu Ala Met Gly Glu
 115 120 125
 Tyr Ser Thr Val Ala Gly Gly Ala Asn Asn Gln Ala Lys Gly Asn Tyr
 130 135 140
 Ser Thr Val Gly Gly Gly Asn Gly Asn Lys Ala Ile Gly Asn Asn Ser
 145 150 155 160
 Thr Val Val Gly Gly Ser Asn Asn Gln Ala Lys Gly Glu His Ser Thr
 165 170 175
 Ile Ala Gly Gly Lys Asn Asn Gln Ala Thr Gly Asn Gly Ser Phe Ala
 180 185 190
 Ala Gly Val Glu Asn Lys Ala Asp Ala Asn Asn Ala Val Ala Leu Gly
 195 200 205

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Asn Lys Asn Thr Ile Glu Gly Thr Asn Ser Val Ala Ile Gly Ser Asn
 210 215 220
 5 Asn Thr Val Lys Thr Gly Lys Glu Asn Val Phe Ile Leu Gly Ser Asn
 225 230 235 240
 Thr Asn Thr Glu Asn Ala Gln Ser Gly Ser Val Leu Leu Gly Asn Asn
 245 250 255
 10 Thr Ala Gly Lys Ala Ala Thr Thr Val Asn Asn Ala Glu Val Asn Gly
 260 265 270
 Leu Thr Leu Glu Asn Phe Ala Gly Ala Ser Lys Ala Asn Ala Asn Asn
 275 280 285
 15 Ile Gly Thr Val Ser Val Gly Ser Glu Asn Asn Glu Arg Gln Ile Val
 290 295 300
 20 Asn Val Gly Ala Gly Gln Ile Ser Ala Thr Ser Thr Asp Ala Val Asn
 305 310 315 320
 Gly Ser Gln Leu His Ala Leu Ala Lys Ala Val Ala Lys Asn Lys Ser
 325 330 335
 25 Asp Ile Lys Gly Leu Asn Lys Gly Val Lys Glu Leu Asp Lys Glu Val
 340 345 350
 Gly Val Leu Ser Arg Asp Ile Asn Ser Leu His Asp Asp Val Ala Asp
 355 360 365
 30 Asn Gln Asp Ser Ile Ala Lys Asn Lys Ala Asp Ile Lys Gly Leu Asn
 370 375 380
 35 Lys Glu Val Lys Glu Leu Asp Lys Glu Val Gly Val Leu Ser Arg Asp
 385 390 395 400
 Ile Gly Ser Leu His Asp Asp Val Ala Asp Asn Gln Asp Ser Ile Ala
 405 410 415
 40 Lys Asn Lys Ala Asp Ile Lys Gly Leu Asn Lys Glu Val Lys Glu Leu
 420 425 430
 Asp Lys Glu Val Gly Val Leu Ser Arg Asp Ile Gly Ser Leu His Asp
 435 440 445
 Asp Val Ala Thr Asn Gln Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile
 450 455 460
 50 Lys Thr Leu Glu Asn Asn Val Glu Glu Glu Leu Leu Asn Leu Ser Gly
 465 470 475 480
 Arg Leu Ile Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile
 485 490 495
 55 Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr
 500 505 510

Leu Lys Asn Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu
 515 520 525
 5 Ile Asp Gln Lys Ala Asp Leu Thr Lys Asp Ile Lys Thr Leu Lys Asn
 530 535 540
 Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln
 545 550 555 560
 10 Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr
 565 570 575
 Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln Tyr Ala
 580 585 590
 15 Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser Ser Ala
 595 600 605
 20 Asn Thr Asp Arg Ile Ala Thr Ala Glu Leu Gly Ile Ala Glu Asn Lys
 610 615 620
 Lys Asp Ala Gln Ile Ala Lys Ala Gln Ala Asn Glu Asn Lys Asp Gly
 625 630 635 640
 25 Ile Ala Lys Asn Gln Ala Asp Ile Gln Leu His Asp Lys Lys Ile Thr
 645 650 655
 Asn Leu Gly Ile Leu His Ser Met Val Ala Arg Ala Val Gly Asn Asn
 660 665 670
 30 Thr Gln Gly Val Ala Thr Asn Lys Ala Asp Ile Ala Lys Asn Gln Ala
 675 680 685
 35 Asp Ile Ala Asn Asn Ile Lys Asn Ile Tyr Glu Leu Ala Gln Gln Gln
 690 695 700
 Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Val Ser Ala Ala
 705 710 715 720
 40 Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Glu Ala Asp Ala Ser Phe
 725 730 735
 Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Gln Gly Glu Ala
 740 745 750
 45 Leu Val Glu Gln Asn Lys Ala Ile Asn Gln Glu Leu Glu Gly Phe Ala
 755 760 765
 50 Ala His Ala Asp Val Gln Asp Lys Gln Ile Leu Gln Asn Gln Ala Asp
 770 775 780
 Ile Thr Thr Asn Lys Thr Ala Ile Glu Gln Asn Ile Asn Arg Thr Val
 785 790 795 800
 55 Ala Asn Gly Phe Glu Ile Glu Lys Asn Lys Ala Gly Ile Ala Thr Asn
 805 810 815

Lys Gln Glu Leu Ile Leu Gln Asn Asp Arg Leu Asn Gln Ile Asn Glu
 820 825 830
 5 Thr Asn Asn His Gln Asp Gln Lys Ile Asp Gln Leu Gly Tyr Ala Leu
 835 840 845
 Lys Glu Gln Gly Gln His Phe Asn Asn Arg Ile Ser Ala Val Glu Arg
 850 855 860
 10 Gln Thr Ala Gly Gly Ile Ala Asn Ala Ile Ala Ile Ala Thr Leu Pro
 865 870 875 880
 Ser Pro Ser Arg Ala Gly Glu His His Val Leu Phe Gly Ser Gly Tyr
 885 890 895
 15 His Asn Gly Gln Ala Ala Val Ser Leu Gly Ala Ala Gly Leu Ser Asp
 900 905 910
 Thr Gly Lys Ser Thr Tyr Lys Ile Gly Leu Ser Trp Ser Asp Ala Gly
 915 920 925
 Gly Leu Ser Gly Gly Val Gly Gly Ser Tyr Arg Trp Lys
 930 935 940
 25

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3538 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TTCTGTGAGC AAATGACTGG CGTAAATGAC TGATGAGTGT CTATTTAATG AAAGATATCA 60
 ATATATAAAA GTTGACTATA GCGATGCAAT ACAGTAAAAT TTGTTACGGC TAAACATAAC 120
 40 GACGGTCCAA GATGGCGGAT ATCGCCATTT ACCAACCTGA TAATCAGTTT GATAGCCATT 180
 AGCGATGGCA TCAAGTTGTG TTGTTGTATT GTCATATAAA CGGTAAATTT GGTGGGTGG 240
 45 ATGCCCCATC TGATTTACCG TCCCCCTAAT AAGTGAGGGG GGGGGGGAGA CCCCAGTCAT 300
 TTATTAGGAG ACTAAGATGA ACAAATTTA TAAAGTGAAA AAAAATGCCG CAGGTCACTT 360
 GGTGGCGTGT TCTGAATTTG CCAAAGGTCA TACCAGGAG GCAGTTTTGG GCAGTTTATT 420
 50 GATTGTTGGA ATATTGGGTA TGGCAACGAC AGCATCTGCA CAAATGGCAA CGACGCCGTC 480
 TGCACAAGTA GTCAAGACAA ACAATAAAAA AAACGGCAGC CACCCTTTCA TCGGTGGTGG 540
 55 CGATTATAAT ACCACCAAAG GCAATTACCC TACCATCGGT GGTGGCCATT TTAATACCGC 600
 CGAAGGCAAT TACTCTACCG TCGGTGGTGG CTTTACTAAC GAAGCCATAG GCAAGAACTC 660

	TACCGTCGGT GGTGGCTTTA CTAACGAAGC CATGGGCGAA TACTCAACCG TCGCAGGCGG	720
5	TGCTAACAAAC CAAGCCAAAG GCAATTACTC TACCGTCGGT GGTGGCAATG GCAACAAAGC	780
	CATAGGCAAC AACTCAACGG TTGTAGGTGG TTCTAACAAAC CAAGCCAAAG GCGAGCACTC	840
	TACCATCGCA GGGGGCAAGA ATAACCAAGC TACAGGTAAT GGTTCATTG CAGCAGGTGT	900
10	AGAGAACAAA GCCGATGCTA ACAACGCCGT CGCTCTAGGT AACAAGAACA CCATCGAAGG	960
	TACAAACTCA GTAGCCATCG GCTCTAATAA TACCGTTAAA ACTGGCAAAG AAAATGTCTT	1020
15	TATTCTTGGC TCTAACACAA ACACAGAAAA TGCACAAAGT GGCTCCGTGC TGCTGGGTAA	1080
	TAATACCGCT GGCAAAGCAG CGACCACTGT TAACAATGCC GAAGTGAACG GCTTAACCCCT	1140
	AGAAAATTTT GCAGGTGCAT CAAAAGCTAA TGCTAATAAT ATTGGTACTG TATCTGTCGG	1200
20	TAGTGAGAAT AATGAGCGTC AAATCGTTAA TGTTGGTGCA GGTCAGATCA GTGCCACCTC	1260
	AACAGATGCT GTTAATGGCT CACAGCTACA TGCTTTAGCC AAAGCTGTTG CTAAAAACAA	1320
25	ATCTGACATC AAAGGTCTTA ATAAGGGGGT GAAAGAGCTT GATAAGGAGG TGGGTGTATT	1380
	AAGCCGAGAC ATTAATTCAC TTCATGATGA TGTTGCTGAC AACCAAGATA GCATTGCTAA	1440
	AAACAAAGCT GACATCAAAG GTCTTAATAA GGAGGTGAAA GAGCTTGATA AGGAGGTGGG	1500
30	TGTATTAAGC CGAGACATTG GTTCACTTCA TGATGATGTT GCTGACAACC AAGATAGCAT	1560
	TGCTAAAAAC AAAGCTGACA TCAAAGGTCT TAATAAGGAG GTGAAAGAGC TTGATAAGGA	1620
35	GGTGGGTGTA TTAAGCCGAG ACATTGGTTC ACTTCATGAT GATGTTGCCA CCAACCAAGC	1680
	TGACATTGCT AAAAACCAAG CGGATATCAA AACACTTGAA AACAATGTCG AAGAAGAATT	1740
	ATTAAATCTA AGCGGTGCGC TCATTGATCA AAAAGCGGAT ATTGATAATA ACATCAACAA	1800
40	TATCTATGAG CTGGCACAAC AGCAAGATCA GCATAGCTCT GATATCAAAA CACTTAAAAA	1860
	CAATGTCGAA GAAGGTTTGT TGGATCTAAG CGGTCGCCTC ATTGATCAAA AAGCAGATCT	1920
45	TACGAAAGAC ATCAAAACAC TTAAAAACAA TGTCGAAGAA GGTTTATTGG ATCTAAGCGG	1980
	TCGCCTCATT GATCAAAAAG CAGATATTGC TAAAAACCA GCTGACATTG CTCAAAACCA	2040
	AACAGACATC CAAGATCTGG CCGCTTACAA CGAGCTACAA GACCAGTATG CTCAAAAGCA	2100
50	AACCGAAGCG ATTGACGCTC TAAATAAAGC AAGCTCTGCC AATACTGATC GTATTGCTAC	2160
	TGCTGAATTG GGTATCGCTG AGAACAAAAA AGACGCTCAG ATCGCCAAAG CACAAGCCAA	2220
55	TGAAAAATAA GACGGCATTG CTAAAAACCA AGCTGATATC CAGTTGCACG ATAAAAAAT	2280
	CACCAATCTA GGTATCCTTC ACAGCATGGT TGCAAGAGCG GTAGGAAATA ATACACAAGG	2340

TGTGCTACC AACAAAGCTG ATATTGCTAA AAACCAAGCA GATATTGCTA ATAACATCAA 2400
 AAATATCTAT GAGCTGGCAC AACAGCAAGA TCAGCATAGC TCTGATATCA AAACCTTGGC 2460
 5 AAAAGTAAGT GCTGCCAATA CTGATCGTAT TGCTAAAAAC AAAGCTGAAG CTGATGCAAG 2520
 TTTTGAAACG CTCACCAAAA ATCAAAATAC TTTGATTGAG CAAGGTGAAG CATTGGTTGA 2580
 10 GCAAAATAAA GCCATCAATC AAGAGCTTGA AGGGTTTGCG GCTCATGCAG ATGTTCAAGA 2640
 TAAGCAAATT TTACAAAACC AAGCTGATAT CACTACCAAT AAGACCGCTA TTGAACAAAA 2700
 TATCAATAGA ACTGTTGCCA ATGGGTTTGA GATTGAGAAA AATAAAGCTG GTATTGCTAC 2760
 15 CAATAAGCAA GAGCTTATTC TTCAAAATGA TCGATTAAAT CAAATTAATG AGACAAATAA 2820
 TCATCAGGAT CAGAAGATTG ATCAATTAGG TTATGCACTA AAAGAGCAGG GTCAGCATTT 2880
 TAATAATCGT ATTAGTGCTG TTGAGCGTCA AACAGCTGGA GGTATTGCAA ATGCTATCGC 2940
 20 AATTGCAACT TTACCATCGC CCAGTAGAGC AGGTGAGCAT CATGTCTTAT TTGGTTCAGG 3000
 TTATCACAAT GGTCAAGCTG CGGTATCATT GGGCGCGGCT GGATTAAGTG ATACAGGAAA 3060
 25 ATCAACTTAT AAGATTGGTC TAAGCTGGTC AGATGCAGGT GGATTATCTG GTGGTGTGG 3120
 TGGCAGTTAC CGCTGGAAAT AGAGCCTAAA TTAACTGCT GTATCAAAAA ATATGGTCTG 3180
 TATAACAGA CCATATTTTT ATCTAAAAAA CTTATCTTAA CTTTTATGAA GCATCATAAG 3240
 30 CCAAAGCTGA GTAATAATAA GAGATGTAA AATAAGAGAT GTTAAACTG CTAAACAATC 3300
 GGCTTGCGAC GATAAAATAA AATACCTGGA ATGGACAGCC CCAAACCAA TGCTGAGATG 3360
 35 ATAAAAATCG CCTCAAAAAA ATGACGCATC ATAACGATAA ATAAATCCAT ATCAATCCA 3420
 AAATAGCCAA TTTGTACCAT GCTAACCATG GCTTTATAGG CAGCGATTCC CGGCATCATA 3480
 CAAATCAAGC TAGGTACAAT CAAGGCTTTA GCGGCAGGC CATGACGCTG AGCAAAAA 3538
 40

(2) INFORMATION FOR SEQ ID NO: 11:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 610 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Lys Leu Leu Pro Leu Lys Ile Ala Val Thr Ser Ala Met Ile Ile
 1 5 10 15
 55 Gly Leu Gly Ala Ala Ser Thr Ala Asn Ala Gln Ser Arg Asp Arg Ser
 20 25 30

	Leu	Glu	Asp	Ile	Gln	Asp	Ser	Ile	Ser	Lys	Leu	Val	Gln	Asp	Asp	Ile	
			35					40						45			
5	Asp	Thr	Leu	Lys	Gln	Asp	Gln	Gln	Lys	Met	Asn	Lys	Tyr	Leu	Leu	Leu	
			50				55					60					
	Asn	Gln	Leu	Ala	Asn	Thr	Leu	Ile	Thr	Asp	Glu	Leu	Asn	Asn	Asn	Val	
	65					70				75					80		
10	Ile	Lys	Asn	Thr	Asn	Ser	Ile	Glu	Ala	Leu	Gly	Asp	Glu	Ile	Gly	Trp	
					85					90					95		
	Leu	Glu	Asn	Asp	Ile	Ala	Asp	Leu	Glu	Glu	Gly	Val	Glu	Glu	Leu	Thr	
15					100				105					110			
	Lys	Asn	Gln	Asn	Thr	Leu	Ile	Glu	Lys	Asp	Glu	Glu	His	Asp	Arg	Leu	
			115					120					125				
20	Ile	Ala	Gln	Asn	Gln	Ala	Asp	Ile	Gln	Thr	Leu	Glu	Asn	Asn	Val	Val	
		130					135					140					
	Glu	Glu	Leu	Phe	Asn	Leu	Ser	Gly	Arg	Leu	Ile	Asp	Gln	Glu	Ala	Asp	
	145					150					155					160	
25	Ile	Ala	Lys	Asn	Asn	Ala	Ser	Ile	Glu	Glu	Leu	Tyr	Asp	Phe	Asp	Asn	
					165					170					175		
	Glu	Val	Ala	Glu	Arg	Ile	Gly	Glu	Ile	His	Ala	Tyr	Thr	Glu	Glu	Val	
30					180				185					190			
	Asn	Lys	Thr	Leu	Glu	Asn	Leu	Ile	Thr	Asn	Ser	Val	Lys	Asn	Thr	Asp	
			195					200					205				
35	Asn	Ile	Asp	Lys	Asn	Lys	Ala	Asp	Ile	Asp	Asn	Asn	Ile	Asn	His	Ile	
		210					215					220					
	Tyr	Glu	Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser	Ser	Asp	Ile	Lys	Thr	
	225					230					235					240	
40	Leu	Lys	Asn	Asn	Val	Glu	Glu	Gly	Leu	Leu	Glu	Leu	Ser	Gly	His	Leu	
					245					250					255		
	Ile	Asp	Gln	Lys	Ala	Asp	Leu	Thr	Lys	Asp	Ile	Lys	Ala	Leu	Glu	Ser	
45					260				265					270			
	Asn	Val	Glu	Glu	Gly	Leu	Leu	Asp	Leu	Ser	Gly	Arg	Leu	Leu	Asp	Gln	
			275					280					285				
50	Lys	Ala	Asp	Leu	Thr	Lys	Asp	Ile	Lys	Ala	Leu	Glu	Ser	Asn	Val	Glu	
		290					295					300					
	Glu	Gly	Leu	Leu	Asp	Leu	Ser	Gly	Arg	Leu	Leu	Asp	Gln	Lys	Ala	Asp	
	305					310					315					320	
55	Ile	Ala	Gln	Asn	Gln	Thr	Asp	Ile	Gln	Asp	Leu	Ala	Ala	Tyr	Asn	Glu	
					325					330					335		

Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu
 340 345 350
 Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala
 5 355 360 365
 Tyr Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile
 370 375 380
 Asp Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys
 10 385 390 395 400
 Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
 15 405 410 415
 Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala
 420 425 430
 Ser Ala Ala Asn Thr Asn Arg Ile Ala Thr Ala Glu Leu Gly Ile Ala
 20 435 440 445
 Glu Asn Lys Lys Asp Ala Gln Ile Ala Lys Ala Gln Ala Asn Ala Asn
 450 455 460
 Lys Thr Ala Ile Asp Glu Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala
 25 465 470 475 480
 Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn
 485 490 495
 Ala Lys Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly
 30 500 505 510
 Arg Val Thr Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly Arg Ile
 35 515 520 525
 Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala Ala
 530 535 540
 Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala Thr
 40 545 550 555 560
 Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly Ala
 565 570 575
 Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala Ile
 45 580 585 590
 Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn Tyr
 50 595 600 605
 Glu Phe
 610

55

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2673 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

10	CCATCAGTAC ATACGCCGCA CCTGACCGAG ACGCTCCGCC AAATCAATGC GTCGGTGTAC	60
	TACGCCCCGA CCGAGCTATG CACGGATAAT GGTGCGATGA TCGCTTACGC TGGCTTTTGT	120
	CGGCTAAGCC GTGGACAGTC GGATGACTTG GCGGTTTCGCT GCATTCCCCG ATGGGATATG	180
15	ACAACGCTTG GCGTATCTGC TCATAGATAG CCACATCAAT CATACCAACG ATATTGGTAT	240
	ATACCAAATT GATACCTGCC AAAAATACCA TATTGAAAGT AGGGTTTGGG TATTATTTAT	300
20	GTAACCTATA TCTAATTTGG TGTGATACT TTGATAAAGC CTTGCTATAC TGTAACCTAA	360
	ATGGATATGA TAGAGATTTT TCCATTTATG CCAGCAAAAAG AGATAGATAG ATAGATAGAT	420
	AGATAGATAG ATAGATAGAT AGATAGATAG ATAGATAAAA CTCTGTCTTT TATCTGTCCA	480
25	CTGATGCTTT CTGCCTGCCA CCGATGATAT CGTTTATCTG CTTTTTTAGG CATCAGTTAT	540
	TTCACCGTGA TGA CTGATGT GATGACTTAA CCACCAAAAAG AGAGTGCTAA ATGAAAACCA	600
	TGAAACTTCT CCCTCTAAAA ATCGCTGTAA CCAGTGCCAT GATTATTGGT TTGGGTGCGG	660
30	CATCTACTGC GAATGCACAG TCTCGGGATA GATCTTTAGA AGATATACAA GATTCAATTA	720
	GTAAACTTGT TCAAGATGAT ATAGATACAC TAAAACAAGA TCAGCAGAAG ATGAACAAGT	780
35	ATCTGTTGCT CAACCAGTTA GCTAATACTT TAATTACAGA CGAGCTCAAC AATAATGTTA	840
	TAAAAAACAC CAATTCTATT GAAGCTCTTG GTGATGAGAT TGGATGGCTT GAAAATGATA	900
	TTGCAGACTT GGAAGAAGGT GTTGAAGAAC TCACCAAAAA CCAAATACT TTGATTGAAA	960
40	AAGATGAAGA GCATGACAGA TTAATCGCTC AAAATCAAGC TGATATCCAA ACACTTGAAA	1020
	ACAATGTCGT AGAAGAATA TTCAATCTAA GCGGTCGCCT AATTGATCAA GAAGCGGATA	1080
45	TTGCTAAAAA TAATGCTTCT ATTGAAGAGC TTTATGATTT TGATAATGAG GTTGCAGAAA	1140
	GGATAGGTGA GATACATGCT TATACTGAAG AGGTAAATAA AACTCTTGAA AACTTGATAA	1200
	CAAACAGTGT TAAGAATACT GATAATATTG ACAAAAACAA AGCTGATATT GATAATAACA	1260
50	TCAACCATAT CTATGAGCTG GCACAACAGC AAGATCAGCA TAGCTCTGAT ATCAAAACAC	1320
	TTAAAAACAA TGTCTGAAGAA GGTGTTGTTG AGCTAAGCGG TCACCTCATT GATCAAAAAG	1380
55	CGGATCTTAC AAAAGACATC AAAGCACTTG AAAGCAATGT CGAAGAAGGT TTGTTGGATC	1440
	TAAGCGGTCG TCTGCTTGAT CAAAAAGCGG ATCTTACAAA AGACATCAAA GCACTTGAAA	1500

5 GCAATGTCGA AGAAGGTTTG TTGGATCTAA GCGGTCGTCT GCTTGATCAA AAAGCGGATA 1560
 TTGCTCAAAA CCAAACAGAC ATCCAAGATC TGGCCGCTTA CAACGAGCTA CAAGACCACT 1620
 ATGCTCAAAA GCAAACCGAA GCGATTGACG CTCTAAATAA AGCAAGCTCT GAGAATACAC 1680
 AAAACATCGA AGATCTGGCC GCTTACAATG AGCTACAAGA TGCCTATGCC AAACAGCAAA 1740
 10 CCGAAGCGAT TGACGCTCTA AATAAAGCAA GCTCTGAGAA TACACAAAAC ATTGCTAAAA 1800
 ACCAAGCGGA TATTGCTAAT AACATCAACA ATATCTATGA GCTGGCACA CAGCAAGATC 1860
 AGCATAGCTC TGATATCAAA ACCTTGCCAA AAGCAAGTGC TGCCAATACT AATCGTATTG 1920
 15 CTACTGCTGA ATTGGGCATC GCTGAGAACA AAAAAGACGC TCAGATCGCC AAAGCACAAAG 1980
 CGAATGCCAA CAAAACGCG ATTGATGAAA ACAAAGCATC TGCGGATACC AAGTTTGCAG 2040
 20 CAACAGCAGA CGCCATTACC AAAAATGGAA ATGCTATCAC TAAAAACGCA AAATCTATCA 2100
 CTGATTGGG CACTAAAGTG GATGGTTTTG ACGGTCGTGT AACTGCATTA GACACCAAAG 2160
 TCAATGCCTT TGATGGTCGT ATCACAGCTT TAGACAGTAA AGTTGAAAAC GGTATGGCTG 2220
 25 CCCAAGCTGC CCTAAGTGGT CTATTCCAGC CTTATAGCGT TGGTAAGTTT AATGCGACCG 2280
 CTGCACTTGG TGGCTATGGC TCAAAATCTG CGGTTGCTAT CGGTGCTGGC TATCGTGTGA 2340
 30 ATCCAAATCT GCGGTTTAAA GCTGGTGCGG CGATTAATAC CAGTGGCAAT AAAAAAGGCT 2400
 CTTATAACAT CGGTGTGAAT TACGAGTTCT AATTGTCTAT CATCACCAAA AAAAGCAGTC 2460
 AGTTTACTGG CTGCTTTTTT ATGGGTTTTT GTGGCTTTTG GTTGTGAGTG ATGGATAAAA 2520
 35 GCTTATCAAG CGATTGATGA ATATCAATAA ATGATTGGTA AATATCAATA AAGCGGTTTA 2580
 GGGTTTTTGG ATATCTTTTA ATAAGTTTAA AAACCCCTGC ATAAAATAAA GCTGGGCATC 2640
 40 AGAGCTGCGA GTAGCGGCAT ACAGCGGGAG ATC 2673

(2) INFORMATION FOR SEQ ID NO: 13:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 873 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 50
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 Met Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Leu Val
 1 5 10 15
 55 Ala Cys Ser Glu Phe Ala Lys Gly His Thr Lys Lys Ala Val Leu Gly
 20 25 30

Ser Leu Leu Ile Val Gly Ile Leu Gly Met Ala Thr Thr Ala Ser Ala
 35 40 45
 5 Gln Gln Thr Ile Ala Arg Gln Gly Lys Gly Met His Ser Ile Ile Gly
 50 55 60
 Gly Gly Asn Asp Asn Glu Ala Asn Gly Asp Tyr Ser Thr Val Ser Gly
 65 70 75 80
 10 Gly Asp Tyr Asn Glu Ala Lys Gly Asp Ser Ser Thr Ile Gly Gly Gly
 85 90 95
 15 Tyr Tyr Asn Glu Ala Asn Gly Asp Ser Ser Thr Ile Gly Gly Gly Phe
 100 105 110
 Tyr Asn Glu Ala Lys Gly Glu Ser Ser Thr Ile Gly Gly Gly Asp Asn
 115 120 125
 20 Asn Ser Ala Thr Gly Met Tyr Ser Thr Ile Gly Gly Gly Asp Asn Asn
 130 135 140
 Ser Ala Thr Gly Arg Tyr Ser Thr Ile Ala Gly Gly Trp Leu Asn Gln
 145 150 155 160
 25 Ala Thr Gly His Ser Ser Thr Val Ala Gly Gly Trp Leu Asn Gln Ala
 165 170 175
 30 Thr Asn Glu Asn Ser Thr Val Gly Gly Gly Arg Phe Asn Gln Ala Thr
 180 185 190
 Gly Arg Asn Ser Thr Val Ala Gly Gly Tyr Lys Asn Lys Ala Thr Gly
 195 200 205
 35 Val Asp Ser Thr Ile Ala Gly Gly Arg Asn Asn Gln Ala Asn Gly Ile
 210 215 220
 Gly Ser Phe Ala Ala Gly Ile Asp Asn Gln Ala Asn Ala Asn Asn Thr
 225 230 235 240
 40 Val Ala Leu Gly Asn Lys Asn Ile Ile Lys Gly Lys Asp Ser Val Ala
 245 250 255
 Ile Gly Ser Asn Asn Thr Val Glu Thr Gly Lys Glu Asn Val Phe Ile
 260 265 270
 45 Leu Gly Ser Asn Thr Lys Asp Ala His Ser Asn Ser Val Leu Leu Gly
 275 280 285
 50 Asn Glu Thr Thr Gly Lys Ala Ala Thr Thr Val Glu Asn Ala Lys Val
 290 295 300
 Gly Gly Leu Ser Leu Thr Gly Phe Val Gly Ala Ser Lys Ala Asn Thr
 305 310 315 320
 55 Asn Asn Gly Thr Val Ser Val Gly Lys Gln Gly Lys Glu Arg Gln Ile
 325 330 335

Val Asn Val Gly Ala Gly Gln Ile Arg Ala Asp Ser Thr Asp Ala Val
 340 345 350

5 Asn Gly Ser Gln Leu His Ala Leu Ala Thr Ala Val Asp Ala Glu Phe
 355 360 365

Arg Thr Leu Thr Gln Thr Gln Asn Ala Leu Ile Glu Gln Gly Glu Ala
 370 375 380

10 Ile Asn Gln Glu Leu Glu Gly Leu Ala Asp Tyr Thr Asn Ala Gln Asp
 385 390 395 400

Glu Lys Ile Leu Lys Asn Gln Thr Asp Ile Thr Ala Asn Lys Thr Ala
 405 410 415

15 Ile Glu Gln Asn Phe Asn Arg Thr Val Thr Asn Gly Phe Glu Ile Glu
 420 425 430

Lys Asn Lys Ala Gly Ile Ala Lys Asn Gln Ala Asp Ile Gln Thr Leu
 435 440 445

Glu Asn Asp Val Gly Lys Glu Leu Leu Asn Leu Ser Gly Arg Leu Leu
 450 455 460

25 Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Asn Ile Tyr Glu Leu
 465 470 475 480

Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Lys Asn
 485 490 495

30 Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln
 500 505 510

Lys Ala Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Asn Asn Val Glu
 515 520 525

Glu Gly Leu Leu Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp
 530 535 540

40 Ile Ala Lys Asn Gln Ala Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu
 545 550 555 560

Leu Gln Asp Gln Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu
 565 570 575

Asn Lys Ala Ser Ser Ala Asn Thr Asp Arg Ile Ala Thr Ala Glu Leu
 580 585 590

50 Gly Ile Ala Glu Asn Lys Lys Asp Ala Gln Ile Ala Lys Ala Gln Ala
 595 600 605

Asn Glu Asn Lys Asp Gly Ile Ala Lys Asn Gln Ala Asp Ile Ala Asn
 610 615 620

55 Asn Ile Lys Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
 625 630 635 640

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Ser Asp Ile Lys Thr Leu Ala Lys Val Ser Ala Ala Asn Thr Asp Arg
 645 650 655
 5 Ile Ala Lys Asn Lys Ala Glu Ala Asp Ala Ser Phe Glu Thr Leu Thr
 660 665 670
 Lys Asn Gln Asn Thr Leu Ile Glu Gln Gly Glu Ala Leu Val Glu Gln
 675 680 685
 10 Asn Lys Ala Ile Asn Gln Glu Leu Glu Gly Phe Ala Ala His Ala Asp
 690 695 700
 Val Gln Asp Lys Gln Ile Leu Gln Asn Gln Ala Asp Ile Thr Ala Asn
 705 710 715 720
 15 Lys Thr Ala Ile Glu Gln Asn Ile Asn Arg Thr Val Ala Asn Gly Phe
 725 730 735
 20 Glu Ile Glu Lys Asn Lys Ala Gly Ile Ala Thr Asn Lys Gln Glu Leu
 740 745 750
 Ile Leu Gln His Asp Arg Leu Asn Arg Ile Asn Glu Thr Asn Asn Arg
 755 760 765
 25 Gln Asp Gln Lys Ile Asp Gln Leu Gly Tyr Ala Leu Lys Glu Gln Gly
 770 775 780
 Gln His Phe Asn Asn Arg Ile Ser Ala Val Glu Arg Gln Thr Ala Gly
 785 790 795 800
 30 Gly Ile Ala Asn Ala Ile Ala Ile Ala Thr Leu Pro Ser Pro Ser Arg
 805 810 815
 35 Ala Gly Glu His His Val Leu Phe Gly Ser Gly Tyr His Asn Gly Gln
 820 825 830
 Ala Ala Val Ser Leu Gly Ala Ala Gly Leu Ser Asp Thr Gly Lys Ser
 835 840 845
 40 Thr Tyr Lys Ile Gly Leu Ser Trp Ser Asp Ala Gly Gly Leu Ser Gly
 850 855 860
 Gly Val Gly Gly Ser Tyr Arg Trp Lys
 865 870
 45

(2) INFORMATION FOR SEQ ID NO: 14:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

	GTAAATGACT GATGAGTGTC TATTTAATGA AAGATACAAT ATATAAAAGT TGACTATAGC	60
	GATGCAATAC AGTAAAATTT GTTACGGCTA AACATAACGA CGGTCCAAGA TGGCGGATAT	120
5	CGCCATTTAC CAACCTGATA ATCAGTTTGA TAGCCATTAG CGATGGCATC AAGTTGTGTT	180
	GTTGTATTGT CATATAAACG GTAAATTTGG TTTGGTGGAT GCCCCATCTG ATTTACCGTC	240
10	CCCCTAATAA GTGAGAGGGG GGGGGAGACC CCAGTCATTT ATTAGGAGAC TAAGATGAAC	300
	AAAATTTATA AAGTGAAAAA AAATGCCGCA GGTCACCTGG TGGCATGTTC TGAATTTGCC	360
	AAAGGCCATA CCAAGAAGGC AGTTTTGGGC AGTTTATTGA TTGTTGGAAT ATTGGGTATG	420
15	GCAACGACAG CATCTGCACA ACAAACAATC GCACGCCAAG GCAAAGGCAT GCACTCTATC	480
	ATCGGTGGTG GCAATGACAA CGAAGCCAAC GGCGATTACT CTACCGTCAG TGGTGGCGAT	540
20	TATAACGAAG CCAAAGGCGA TAGCTCTACC ATCGGTGGTG GCTATTATAA CGAAGCCAAC	600
	GGCGATAGCT CTACCATCGG TGGTGGCTTT TATAACGAAG CCAAAGGCGA GAGCTCTACC	660
	ATCGGTGGTG GCGATAACAA CTCAGCCACA GGCATGTACT CTACCATCGG TGGTGGCGAT	720
25	AACAACCTAG CCACAGGCAG GTACTCTACC ATCGCAGGGG GTTGGCTTAA CCAAGCTACA	780
	GGTCATAGCT CAACGGTTGC AGGGGGTTGG CTTAACCAAG CTACAAACGA GAATTCTACC	840
30	GTTGGTGGCG GCAGGTTTAA CCAAGCTACA GGTCGTAACCT CAACGGTTGC AGGGGGCTAT	900
	AAAAACAAAG CCACAGGCGT AGACTCTACC ATCGCAGGGG GCAGGAATAA CCAAGCCAAC	960
	GGTATAGGTT CATTTGCAGC AGGTATAGAC AACCAAGCCA ATGCCAACAA CACCGTCGCT	1020
35	CTAGGTAACA AGAACATCAT CAAAGGTAAA GACTCAGTAG CCATCGGCTC TAATAATACC	1080
	GTTGAAACTG GCAAAGAAAA TGTCTTTATT CTTGGCTCTA ACACAAAAGA TGCACATAGT	1140
40	AACTCAGTGC TACTGGGTAA TGAGACCACT GGCAAAGCAG CGACCACTGT TGAGAATGCC	1200
	AAAGTGGGTG GTCTAAGCCT AACAGGATTT GTAGGTGCAT CAAAAGCTAA TACTAATAAT	1260
	GGTACTGTAT CTGTCGGTAA GCAGGGTAAA GAGCGTCAAA TCGTTAATGT TGGTGCAGGT	1320
45	CAGATCCGTG CTGATTCAAC AGATGCTGTT AATGGCTCAC AGCTACATGC TTTGGCCACA	1380
	GCTGTGATG CAGAATTTAG AACACTCACC CAACTCAAA ATGCTTTGAT TGAGCAAGGT	1440
50	GAAGCCATCA ATCAAGAGCT TGAAGGTTTG GCAGATTATA CAAATGCTCA AGATGAGAAA	1500
	ATTCTAAAAA ACCAACTGA CATCACTGCC AATAAACTG CTATTGAGCA AAATTTTAAT	1560
	AGAACTGTTA CCAATGGGTT TGAGATTGAG AAAAATAAAG CTGGTATTGC TAAAAACCA	1620
55	GCGGATATCC AAACACTTGA AAACGATGTC GGAAAAGAAC TATTAAATCT AAGCGGTCGC	1680
	CTGCTTGATC AAAAAGCAGA TATTGATAAT AACATCAACA ATATCTATGA GCTGGCACAA	1740

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CAGCAAGATC AGCATAGCTC TGATATCAAA ACACTTAAAA ACAATGTCGA AGAAGGTTTG 1800
TTGGATCTAA GCGGTCGCCT CATTGATCAA AAAGCAGATC TTACGAAAGA CATCAAAGCA 1860
CTTGAAAACA ATGTCGAAGA AGGTTTATTG GATCTAAGCG GTCGCCTCAT TGATCAAAAA 1920
GCAGATATTG CTAAAAACCA AGCAGACATC CAAGATTTGG CCGCTTACAA CGAGCTACAA 1980
GACCAGTATG CTCAAAGCA AACCGAAGCG ATTGACGCTC TAAATAAAGC AAGCTCTGCC 2040
AATACTGATC GTATTGCTAC TGCTGAATTG GGTATCGCTG AGAACAAAAA AGACGCTCAG 2100
ATCGCCAAAG CACAAGCCAA TGAAAATAAA GACGGCATTG CTAAAAACCA AGCAGATATT 2160
GCTAATAACA TCAAAAATAT CTATGAGCTG GCACAACAGC AAGATCAGCA TAGCTCTGAT 2220
ATCAAACCT TGGCAAAAGT AAGTGCTGCC AATACTGATC GTATTGCTAA AAACAAAGCT 2280
GAAGCTGATG CAAGTTTTGA AACGCTCACC AAAAATCAAA ATACTTTGAT TGAGCAAGGT 2340
GAAGCATTGG TTGAGCAAAA TAAAGCCATC AATCAAGAGC TTGAAGGGTT TGGCGCTCAT 2400
GCAGATGTTT AAGATAAGCA AATTTTACAA AACCAAGCTG ATATCACTGC CAATAAGACC 2460
GCTATTGAAC AAAATATCAA TAGAACTGTT GCCAATGGGT TTGAGATTGA GAAAAATAAA 2520
GCTGGTATTG CTACCAATAA GCAAGAGCTT ATTCTTCAAC ATGATCGATT AAATCGAATT 2580
AATGAGACAA ATAATCGTCA GGATCAGAAG ATTGATCAAT TAGGTTATGC ACTAAAAGAG 2640
CAGGGTCAGC ATTTTAATAA TCGTATTAGT GCTGTTGAGC GTCAAACAGC TGGAGGTATT 2700
GCAAATGCTA TCGCAATTGC AACTTTACCA TCGCCCAGTA GAGCAGGTGA GCATCATGTC 2760
TTATTTGGTT CAGGTTATCA CAATGGTCAA GCTGCGGTAT CATTGGGTGC GGCTGGGTTA 2820
AGTGATACAG GAAAATCAAC TTATAAGATT GGTCTAAGCT GGTGAGATGC AGGTGGATTA 2880
TCTGGTGGTG TTGGTGGTAG TTACCGCTGG AAATAGAGCC TAAATTTAAC TGCTGTATCA 2940
AAAAATATGG TCTGTATAAA CAGACCATAT TTTTATCTAA AAATTATCT TAACTTTTAT 3000
GAAGCATCAT AAGCCAAAGC TGAGTAATAA TAAGAGATGT TAAAATAAGA GATGTTAAAA 3060
CTGCTAAACA ATCGGCTTAC GACGATAAAA TAAAATACCT GGAATGGACA GCCCCAAAC 3120
CAATGCTGAG ATGATAAAAA TCGCCTCAAA AAAATGACGC ATCATAACGA TAAATAAATC 3180
CATATCAAAT CCAAATAGC CAATTTGTAC CATGCTAACC ATGGCTTTAT AGGCAGCGAT 3240
TCCCGGCATC ATACAAATCA AGCTAGGTAC AATCAAGGCT TTAGGCGGCA GG 3292

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 889 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

10

Val Asn Lys Ile Tyr Lys Val Lys Lys Asn Ala Ala Gly His Leu Val
 1 5 10 15

Ala Cys Ser Glu Phe Ala Lys Gly His Thr Lys Lys Ala Val Leu Gly
 20 25 30

15

Ser Leu Leu Ile Val Gly Ala Leu Gly Met Ala Thr Thr Ala Ser Ala
 35 40 45

Gln Pro Leu Val Ser Thr Asn Lys Pro Asn Gln Gln Val Lys Gly Tyr
 50 55 60

20

Trp Ser Ile Ile Gly Ala Gly Arg His Asn Asn Val Gly Gly Ser Ala
 65 70 75 80

His His Ser Gly Ile Leu Gly Gly Trp Lys Asn Thr Val Asn Gly Tyr
 85 90 95

25

Thr Ser Ala Ile Val Gly Gly Tyr Gly Asn Glu Thr Gln Gly Asp Tyr
 100 105 110

30

Thr Phe Val Gly Gly Gly Tyr Lys Asn Leu Ala Lys Gly Asn Tyr Thr
 115 120 125

Phe Val Gly Gly Gly Tyr Lys Asn Leu Ala Glu Gly Asp Asn Ala Thr
 130 135 140

35

Ile Ala Gly Gly Phe Ala Asn Leu Ala Glu Gly Asp Asn Ala Thr Ile
 145 150 155 160

Ala Gly Gly Phe Glu Asn Arg Ala Glu Gly Ile Asp Ser Val Val Ser
 165 170 175

40

Gly Gly Tyr Ala Asn Gln Ala Thr Gly Glu Ser Ser Thr Val Ala Gly
 180 185 190

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Gly Ser Asn Asn Leu Ala Glu Gly Lys Ser Ser Ala Ile Gly Gly Gly
 195 200 205

Arg Gln Asn Glu Ala Ser Gly Asp Arg Ser Thr Val Ser Gly Gly Tyr
 210 215 220

50

Asn Asn Leu Ala Glu Gly Lys Ser Ser Ala Ile Gly Gly Gly Glu Phe
 225 230 235 240

Asn Leu Ala Leu Gly Asn Asn Ala Thr Ile Ser Gly Gly Arg Gln Asn
 245 250 255

55

Glu Ala Ser Gly Asp Arg Ser Thr Val Ala Gly Gly Glu Gln Asn Gln
 260 265 270

Ala Ile Gly Lys Tyr Ser Thr Ile Ser Gly Gly Arg Gln Asn Glu Ala
275 280 285

5 Ser Gly Asp Arg Ser Thr Val Ala Gly Gly Glu Gln Asn Gln Ala Ile
290 295 300

Gly Lys Tyr Ser Thr Val Ser Gly Gly Tyr Arg Asn Gln Ala Thr Gly
305 310 315 320

10 Lys Gly Ser Phe Ala Ala Gly Ile Asp Asn Lys Ala Asn Ala Asp Asn
325 330 335

Ala Val Ala Leu Gly Asn Lys Asn Thr Ile Glu Gly Glu Asn Ser Val
340 345 350

15 Ala Ile Gly Ser Asn Asn Thr Val Lys Lys Asn Gln Lys Asn Val Phe
355 360 365

20 Ile Leu Gly Ser Asn Thr Asp Thr Lys Asp Ala Gln Ser Gly Ser Val
370 375 380

Leu Leu Gly Asp Asn Thr Ser Gly Lys Ala Ala Thr Ala Val Glu Asp
385 390 395 400

25 Ala Thr Val Gly Asp Leu Ser Leu Thr Gly Phe Ala Gly Val Ser Lys
405 410 415

Ala Asn Ser Gly Thr Val Ser Val Gly Ser Glu Gly Lys Glu Arg Gln
420 425 430

30 Ile Val His Val Gly Ala Gly Arg Ile Ser Asn Asp Ser Thr Asp Ala
435 440 445

35 Val Asn Gly Ser Gln Leu Tyr Ala Leu Ala Ala Val Asp Asp Asn
450 455 460

Gln Tyr Asp Ile Glu Lys Asn Gln Asp Asp Ile Ala Lys Asn Gln Ala
465 470 475 480

40 Asp Ile Ala Lys Asn Gln Ala Asp Ile Gln Thr Leu Glu Asn Asp Val
485 490 495

Gly Lys Glu Leu Leu Asn Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala
500 505 510

45 Asp Ile Asp Asn Asn Ile Asn His Ile Tyr Glu Leu Ala Gln Gln Gln
515 520 525

50 Asp Gln His Ser Ser Asp Ile Lys Thr Leu Lys Lys Asn Val Glu Glu
530 535 540

Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu
545 550 555 560

55 Thr Lys Asp Ile Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu
565 570 575

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Asp Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Gln Asn
 580 585 590

5 Gln Ala Asn Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Asp Gln
 595 600 605

Tyr Ala Gln Lys Gln Thr Glu Ala Ile Asp Ala Leu Asn Lys Ala Ser
 610 615 620

10 Ser Glu Asn Thr Gln Asn Ile Glu Asp Leu Ala Ala Tyr Asn Glu Leu
 625 630 635 640

Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp Ala Leu Asn
 15 645 650 655

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn Gln Ala Asp
 660 665 670

20 Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp
 675 680 685

Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser Ala Ala Asn
 690 695 700

25 Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu
 705 710 715 720

Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp Lys Glu His
 30 725 730 735

Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala Asn Lys Ala
 740 745 750

35 Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn
 755 760 765

Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp Leu Gly Thr
 770 775 780

40 Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp Thr Lys Val
 785 790 795 800

Asn Ala Phe Asp Gly Arg Ile Thr Ala Leu Asp Ser Lys Val Glu Asn
 45 805 810 815

Gly Met Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser
 820 825 830

50 Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys
 835 840 845

Ser Ala Val Ala Ile Gly Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala
 850 855 860

55 Phe Lys Ala Gly Ala Ala Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser
 865 870 875 880

Tyr Asn Ile Gly Val Asn Tyr Glu Phe
885

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(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 4228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

20

GCCGCACCCT	GACCGAGACG	CTCCGCCAAA	TCGATGCGTC	GGTGTACTAT	GCCCCGACCG	60
AGCTATGCAC	GGATAATGGT	GCGATGATCG	CCTATGCTGG	CTTTTGTCTGG	CTAAGCCGTG	120
GACAGTCGGA	TGACTTGGTG	GTTGCTGTGA	TTCCCCGATG	GGATATGACG	ACGCTTGGTA	180
TCGAATATGA	TAATTAGGCT	GTGGTATTTG	AGTTTGTAGT	AATGTACCTA	CTACCACTAA	240
TTTATCATAC	AATACATAAA	CATAAAAAAC	ATCGGTATTG	TTAAAAACA	ATACCCAAGT	300
TAAAATAGCT	CAATACTTTA	CCATAGCACA	AAGAACTTG	TGAACGAAAC	ATTTAATAAT	360
TGCCCCAAAT	GTTACTGCAC	ACACTTTGTA	AAAGCAGGCT	TGGGCAATGG	CAAACAACGA	420
TACAAATGCA	AAGGTTGCCA	TCACTATTTT	TCTGTGAAGC	AACGAAGCAA	CCAAAAAAGT	480
AATGACATTA	AAAAACAAG	CCATTGATAC	AAACAGTAAA	CAAATCTTAG	GCTTTGTCTG	540
TGGTAAACA	GACACTAACA	CCTTTAAACG	ACTTTATCAG	CAGTTAAATA	CCCATAGCAT	600
TCAACTGTTT	TTTAGTGACT	ACTGGAAATC	TTATCGTCAA	GTCATTTTAA	AGCCAAAACA	660
TATAACAAGC	AAAGCTCAAA	CTTTTACCAT	AGAGGGCTAT	AATAGTCTCA	TTAGGCATTT	720
CATAGCAAGA	TTTACAAGAA	AGTCAAAGTG	TTATTCTAAA	TCCGAAAAAA	TGATAGAAAA	780
CACGTTGAAT	TTATTATTTG	CTAAGTGGA	TGGTAGCTTA	AGATATGTAT	TTTAATTTAA	840
CAATGCCAAA	AACATCAATT	ACAGTAAGAT	TTTAGGCGTT	TTGCAGTTGC	TACTTTAGTA	900
AAGCTTTGTT	ATACTAGCTG	TTAGTATACT	CAAGCTTGTT	TGTGTTTGAG	CTATATTTAT	960
TTTATAGCAG	TAGTTGGTTA	TAAAATATAA	ATAAAGCTAA	GCTCGAGGGT	TTGGTAATGG	1020
TTTTTTATGT	TTATAATACC	AACAGAGTCT	ATACAGCTAA	AATAGCTAAT	ACCTTAGGTG	1080
TATTACAAGT	AAAAATCCTT	TGGTTAATCA	GGGGGTGTAT	TATATGTATA	TTTCCTTTGT	1140
ATTTGGTTAT	AGCAATCCCT	TGGTAAGAAA	TCATATCTAT	TTTTTATTGT	TCAATTATTT	1200
AGGAGACTAA	GGTGAACAAA	ATTTATAAAG	TGAAAAAAA	TGCCGCAGGT	CACTTGGTGG	1260

55

CATGTTCTGA ATTTGCCAAA GGCCATACCA AAAAGGCAGT TTTGGGCAGT TTATTGATTG 1320
TTGGGGCGTT GGGCATGGCA ACGACGGCGT CTGCACAGCC ATTAGTAAGT ACAAATAAGC 1380
5 CTAATCAGCA GGTAAAGGGT TATTGGTCTA TTATTGGTGC AGGTCGTCAT AATAACGTAG 1440
GTGGATCCGC TCATCACTCA GGGATTCTTG GTGGTTGGAA AAATACAGTC AATGGCTATA 1500
CCTCAGCCAT TGTAGGTGGT TATGGTAACG AAATCAGGG TGATTATACA TTCGTCGGTG 1560
10 GTGGTTATAA AAACCTGGCA AAGGGTAATT ATACATTCGT CGGTGGTGGT TATAAAAACT 1620
TGGCAGAGGG TGATAATGCA ACCATCGCTG GTGGTTTTGC AAACCTGGCA GAGGGTGATA 1680
15 ATGCAACCAT CGCTGGTGGT TTTGAAAACC GTGCAGAGGG TATCGACTCA GTAGTTTCTG 1740
GTGGTTATGC CAACCAAGCT ACAGGAGAAA GCTCAACCGT CGCAGGTGGT TCTAATAACC 1800
TAGCAGAGGG CAAAAGCTCA GCCATTGGTG GTGGCCGTCA AAATGAGGCG TCTGGTGACC 1860
20 GATCTACTGT CTCAGGTGGT TATAATAACC TAGCAGAGGG CAAAAGCTCA GCCATTGGTG 1920
GCGGTGAGTT TAACTTAGCA TTAGGGAATA ACGCTACCAT TAGTGGTGGC CGTCAAAATG 1980
25 AGGCGTCTGG TGACCGATCT ACTGTCGCAG GTGGTGAACA AAACCAAGCC ATAGGCAAGT 2040
ATTCTACCAT TAGTGGTGGC CGTCAAAATG AGGCGTCTGG TGACCGATCT ACTGTCGCAG 2100
GTGGTGAACA AAACCAAGCC ATAGGCAAGT ATTCTACCGT TAGTGGTGGC TATCGAAACC 2160
30 AAGCCACAGG TAAAGGTTCA TTTGCAGCAG GTATAGATAA CAAAGCCAAT GCCGACAACG 2220
CCGTCGCTCT AGGTAACAAG AACACCATCG AAGGTGAAAA CTCAGTAGCC ATCGGCTCTA 2280
35 ATAATACCGT TAAAAAAAAT CAAAAAATG TCTTTATTCT TGGCTCTAAC ACAGACACAA 2340
AAGATGCACA AAGCGGCTCA GTACTGCTAG GTGATAATAC CTCTGGTAAA GCAGCGACCG 2400
CTGTTGAGGA TGCCACAGTG GGTGATCTAA GCCTAACAGG ATTTGCAGGC GTATCAAAAG 2460
40 CTAATAGTGG TACTGTATCT GTCGGTAGTG AGGGTAAAGA GCGTCAAATC GTTCATGTTG 2520
GTGCAGGTCG GATCAGTAAT GATTCAACAG ATGCTGTAA TGGCTCACAG CTATATGCTT 2580
45 TGGCCGCAGC TGTTGATGAC AACCAATATG ACATTGAAAA AAACCAAGAT GACATTGCTA 2640
AAAACCAAGC TGACATTGCT AAAAACCAAG CTGACATCCA AACACTTGAA AACGATGTCTG 2700
GAAAAGAACT ATTAAATCTA AGCGGTCGCC TCATTGATCA AAAAGCAGAT ATTGATAATA 2760
50 ACATCAACCA TATCTATGAG CTGGCACAAC AGCAAGATCA GCATAGCTCT GATATCAAAA 2820
CACTTAAAAA AAATGTCGAA GAAGGTTTGT TGGAGCTAAG CGGTCACCTC ATTGATCAAA 2880
55 AAGCAGATCT TACAAAAGAC ATCAAAGCAC TTGAAAGCAA TGTCGAAGAA GGTTTGTGTTG 2940
ATCTAAGCGG TCGCCTCATT GATCAAAAAG CAGATATTGC TCAAAACCAA GCTAACATCC 3000

SUBSTITUTE SHEET (RULE 26)

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AAGATTTGGC TGCTTACAAC GAGCTACAAG ACCAGTATGC TCAAAAGCAA ACCGAAGCGA 3060
TTGACGCTCT AAATAAAGCA AGCTCTGAGA ATACACAAAA CATCGAAGAT CTGGCCGCTT 3120
ACAACGAGCT ACAAGATGCC TATGCCAAAC AGCAAACCGA AGCCATTGAC GCTCTAAATA 3180
AAGCAAGCTC TGAGAATACA CAAAACATTG CTAAAAACCA AGCGGATATT GCTAATAACA 3240
TCAACAATAT CTATGAGCTA GCACAACAGC AAGATCAGCA TAGCTCTGAT ATCAAAACCT 3300
TGGCAAAAGC AAGTGCTGCC AATACTGATC GTATTGCTAA AAACAAAGCC GATGCTGATG 3360
CAAGTTTTTGA AACGCTCACC AAAAATCAAA ATACTTTGAT TGAAAAAGAT AAAGAGCATG 3420
ACAAATTAAT TACTGCAAAC AAAACTGCGA TTGATGCCAA TAAAGCATCT GCGGATACCA 3480
AGTTTGCAGC GACAGCAGAC GCCATTACCA AAAATGGAAA TGCTATCACT AAAAACGCAA 3540
AATCTATCAC TGATTTGGGT ACTAAAGTGG ATGGTTTTGA CGGTCGTGTA ACTGCATTAG 3600
ACACCAAAGT CAATGCCTTT GATGGTCGTA TCACAGCTTT AGACAGTAAA GTTGAAAACG 3660
GTATGGCTGC CCAAGCTGCC CTAAGTGGTC TATTCCAGCC TTATAGCGTT GGTAAGTTTA 3720
ATGCGACCGC TGCACTTGGT GGCTATGGCT CAAAATCTGC GGTGCTATC GGTGCTGGCT 3780
ATCGTGTGAA TCCAAATCTG GCGTTTAAAG CTGGTGCGGC GATTAATACC AGTGGCAATA 3840
AAAAAGGCTC TTATAACATC GGTGTGAATT ACGAGTTCTA ATTGTCTATC ATCACCAAAA 3900
AAAGCAGTCA GTTTACTGGC TGCTTTTTTA TGGGTTTTTG TGGCTTTTGG TTGTGAGTGA 3960
TGGATAAAAG CTTGTCAAGC GATTGATGAA TATCAATAAA TGATTGGTAA ATATCAATAA 4020
AGCGGTTTAG GGTTTTTTGA TATCTTTTAA TAAGTTTAAA AACCCCTGCA TAAAATAAAG 4080
CTGGCATCAG AGCTGCGAAG TAGCGGCATA CAGCTGGCAA TGCACGCCTG TGCCTAGGGG 4140
GCGTGAGACC ACCCAGCCTT TCGTTCGTA TTCTAAAATT ACCCAATCAG GCAGAGCGGC 4200
AACTCCATGT TCGGAGGCGA CCAGCTGA 4228

45 (2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

55 Ala Gln Gln Gln Asp Gln His
1 5

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Tyr Glu Leu Ala Gln Gln Gln Asp Gln His
1 5 10

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Tyr Asp Leu Ala Gln Gln Gln Asp Gln His
1 5 10

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GACGCTCAAC AGCACTAATA CG

22

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CCAAGCTGAT ATCACTACC

19

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCAATGCCTT TGATGGTC

18

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TGTATGCCGC TACTCGCAGC T

21

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2..13
- (D) OTHER INFORMATION: /note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Asn Xaa Ala Xaa Xaa Tyr Ser Xaa Ile Gly Gly Gly Xaa Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Gln Ala Asp Ile
1

5 (2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
10 (C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

15 Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Val Pro Tyr Ser Val Gly
1 5 10 15

Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys
20 25 30

20

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Gly Lys Ile Thr Lys Asn Ala Ala Arg Gln Glu Asn Gly
1 5 10

35

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

45

Val Ile Gly Asp Leu Gly Arg Lys Val
1 5

50 (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
55 (C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:4

(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Ala Leu Glu Xaa Asn Val Glu Glu Gly Leu

1

5

10

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:11..12

(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Xaa Xaa Leu Ser

1

5

10

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Ala Leu Glu Phe Asn Gly Glu

1

5

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:7

(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Ser Ile Thr Asp Leu Gly Xaa Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:13..15

(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Ser Ile Thr Asp Leu Gly Thr Ile Val Asp Gly Phe Xaa Xaa Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Ser Ile Thr Asp Leu Gly Thr Ile Val Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:5..19

(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Val Asp Ala Leu Xaa Thr Lys Val Asn Ala Leu Asp Xaa Lys Val Asn
1 5 10 15
Ser Asp Xaa Thr
20

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Leu Leu Ala Glu Gln Gln Leu Asn Gly Lys Thr Leu Thr Pro Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Ala Lys His Asp Ala Ala Ser Thr Glu Lys Gly Lys Met Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Asn Gln Asn Thr Leu Ile Glu Lys Thr Ala Asn Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Ile Asp Lys Asn Glu Tyr Ser Ile Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Ser Ile Thr Asp Leu Gly Thr Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Asn Gln Asn Thr Leu Ile Glu Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Ala Leu His Glu Gln Gln Leu Glu Thr Leu Thr Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Asn Ser Ser Asp
1

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu Thr Leu Thr Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Phe Ala Ala Thr Ala Ile Ala Lys Asp Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Arg Leu Leu Asp Gln Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION:12
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION:4..8

(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Ala Lys Ala Xaa Ala Ala Asn Xaa Asp Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala
1 5 10 15

Ala Tyr Asn Glu Leu Gln
20

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
1 5 10 15

Gln Gln Gln Asp Gln
20

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Tyr Asn Glu Arg Gln Thr Glu Ala Ile Asp Ala Leu Asn
1 5 10

5 (2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
10 (C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

15 Ile Leu Gly Asp Thr Ala Ile Val Ser Asn Ser Gln Asp
1 5 10

20 (2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
25 (C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

30 Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly
1 5 10 15

Arg

35 (2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
40 (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

45 Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Glu Leu Ser Gly Arg
1 5 10 15

50 Thr Ile Asp Gln Arg
20

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION:11
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Asn Gln Ala His Ile Ala Asn Asn Ile Asn Xaa Ile Tyr Glu Leu Ala
1 5 10 15

Gln Gln Gln Asp Gln Lys
20

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala
1 5 10 15

Ala Tyr Asn Glu Leu Gln
20

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Ala Thr His Asp Tyr Asn Glu Arg Gln Thr Glu Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Met Ile Leu Gly Asp Thr Ala Ile Val Ser Asn Ser Gln Asp Asn Lys
1 5 10 15

Thr Gln Leu Lys Phe Tyr Lys
20

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 12..13
(D) OTHER INFORMATION: /note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ala Gly Asp Thr Ile Ile Pro Leu Asp Asp Asp Xaa Xaa Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION:8
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Leu Leu His Glu Gln Gln Leu Xaa Gly Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION:5
(D) OTHER INFORMATION:/note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Ile Phe Phe Asn Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His
1 5 10 15
Ser Ser Asp Ile Lys Thr Leu
20

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GGTGCAGGTC AGATCAGTGA C

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GCCACCAACC AAGCTGAC

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

AGCGGTCGCC TGCTTGATCA G

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CTGATCAAGC AGGCGACCGC T

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CAAGATCTGG CCGCTTACAA

20

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

TTGTAAGCGG CCAGATCTTG

20

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TGCATGAGCC GCAAACCC

18

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Leu Leu Ala Glu Gln Gln Leu Asn Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Ala Leu Glu Ser Asn Val Glu Glu Gly Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3788 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Thr His Glu Phe Ile Arg Ser Thr Ser Glu Gln Glu Asn Cys Glu Ser
 1 5 10 15

Ala Arg Glu Asn Thr His Glu Asp Ile Ser Lys Glu Thr Thr Glu Ser
 20 25 30

Ala Asn Asp Ala Thr Leu Glu Ala Ser Thr Ser Met Glu Phe Thr His
 35 40 45

Glu Ser Glu Ala Leu Arg Glu Ala Asp Tyr Asn Thr His Glu Thr Asp
 50 55 60

Arg Ile Val Glu Cys His Glu Cys Lys Trp Ile Thr His Gly Glu Arg
 65 70 75 80

Arg Ile Thr His Glu Ser Glu Ser Glu Gln Glu Asn Cys Glu Ser Ala
 85 90 95

Arg Glu Asn Ala Met Glu Asp Asn Thr His Glu Asp Ile Ser Lys Glu

			100				105				110					
	Thr	Thr	Glu	Ser	Ala	Asn	Asp	His	Ala	Arg	Asp	Cys	Pro	Ile	Glu	Ser
			115					120				125				
5																
	Ala	Thr	Thr	Ala	Cys	His	Glu	Asp	Ala	Ser	Phe	Leu	Leu	Trp	Ser	Ala
			130				135					140				
10	Asn	Asp	Asp	Asn	Thr	His	Ala	Val	Glu	Ala	Asn	Tyr	Ser	Pro	Glu	Cys
	145					150					155				160	
	Ile	Ala	Leu	Cys	His	Ala	Arg	Ala	Cys	Thr	Glu	Arg	Ser	Asp	Asn	Thr
					165					170					175	
15																
	Thr	Arg	Ala	Asn	Ser	Leu	Ala	Thr	Glu	Ala	Asn	Tyr	Ser	Glu	Gln	Glu
				180					185					190		
	Asn	Cys	Glu	Ser	Thr	His	Ala	Thr	Ile	Ser	Thr	His	Glu	Arg	Glu	Ile
20			195					200					205			
	Ser	Asn	Ser	Thr	Ala	Arg	Thr	Cys	Asp	Asn	Ser	Glu	Gln	Ile	Asp	Asn
		210					215					220				
25	Phe	Ile	Leu	Glu	Asn	Ala	Met	Glu	Thr	Tyr	Pro	Glu	Ser	Thr	Arg	Ala
	225					230					235				240	
	Asn	Asp	Thr	Pro	Leu	Gly	Tyr	Ser	Glu	Gln	Ile	Asp	Asn	Glu	Ser	Pro
					245					250				255		
30																
	Ala	Ala	Ala	Pro	Arg	Thr	Glu	Ile	Asn	Asn	Ala	Leu	Ile	Asn	Glu	Ala
				260					265					270		
	Arg	Ser	Glu	Gln	Ile	Asp	Asn	Glu	Ser	Pro	Ala	Asn	Ala	Asp	Asn	Ala
35			275					280				285				
	Asp	Asx	Leu	Glu	Leu	Ile	Asn	Glu	Ala	Arg	Ser	Glu	Gln	Ile	Asp	Asn
		290					295					300				
40	Glu	Ser	Pro	Ala	Ala	Ala	Pro	Arg	Thr	Glu	Ile	Asn	Asn	Ala	Leu	Ile
	305					310					315				320	
	Asn	Glu	Ala	Arg	Ser	Glu	Gln	Ile	Asp	Asn	Glu	Ser	Pro	Ala	Asn	Ala
				325						330				335		
45																
	Asp	Asn	Ala	Asp	Asx	Leu	Glu	Leu	Ile	Asn	Glu	Ala	Arg	Ser	Glu	Gln
			340						345					350		
	Ile	Asp	Asn	Glu	Ser	Pro	Ala	Ala	Ala	Pro	Ala	Thr	Pro	Arg	Thr	Glu
50			355					360					365			
	Ile	Asn	Asn	Ala	Leu	Ile	Asn	Glu	Ala	Arg	Ser	Glu	Gln	Ile	Asp	Asn
		370					375					380				
55	Glu	Ser	Pro	Ala	Asn	Ala	Pro	Ala	Thr	Asp	Asn	Ala	Asp	Asx	Leu	Glu
	385					390					395				400	

SUBSTITUTE SHEET (RULE 26)

Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn Glu Ser Pro Ala
 405 410 415
 Ala Ala Pro Ala Thr Pro Arg Thr Glu Ile Asn Asn Ala Leu Ile Asn
 5 420 425 430
 Glu Ala Arg Ser Glu Gln Ile Asp Asn Glu Ser Pro Ala Asn Ala Pro
 435 440 445
 Ala Thr Asp Asn Ala Asp Asx Leu Glu Leu Ile Asn Glu Ala Arg Ser
 10 450 455 460
 Glu Gln Ile Asp Asn Thr Thr Ala Ser Pro Ala Ala Ala Pro Ala Thr
 465 470 475 480
 Pro Arg Thr Glu Ile Asn Asn Ala Leu Ile Asn Glu Ala Arg Ser Glu
 15 485 490 495
 Gln Ile Asp Asn Thr Thr Ala Ser Pro Ala Asn Ala Pro Ala Thr Asp
 20 500 505 510
 Asn Ala Asp Asx Leu Glu Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile
 515 520 525
 Asp Asn Thr Thr Ala Ser Pro Ala Ala Ala Pro Ala Thr Pro Arg Thr
 25 530 535 540
 Glu Ile Asn Asn Ala Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp
 545 550 555 560
 Asn Thr Thr Ala Ser Pro Ala Asn Ala Pro Ala Thr Asp Asn Ala Asp
 30 565 570 575
 Asx Leu Glu Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn Thr
 35 580 585 590
 Thr Ala Ser Pro Ala Ala Ala Pro Ala Thr Pro Arg Thr Glu Ile Asn
 595 600 605
 Asn Ala Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn Thr Thr
 40 610 615 620
 Ala Ser Pro Ala Asn Ala Pro Ala Thr Asp Asn Ala Asp Asx Leu Glu
 625 630 635 640
 Leu Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn Thr Thr Ala Ser
 645 650 655
 Pro Ala Ala Ala Pro Ala Thr Pro Arg Thr Glu Ile Asn Asn Ala Leu
 50 660 665 670
 Ile Asn Glu Ala Arg Ser Glu Gln Ile Asp Asn Thr Thr Ala Ser Pro
 675 680 685
 Ala Asn Ala Pro Ala Thr Asp Asn Ala Asp Asx Leu Glu Leu Ile Asn
 55 690 695 700

SUBSTITUTE SHEET (RULE 26)

	Glu	Ala	Arg	Ser	Glu	Gln	Ile	Asp	Asn	Thr	His	Arg	Gly	His	Ser	Glu	705	710	715	720
5	Gln	Ile	Asp	Asn	Ile	Ser	Gly	Ile	Val	Glu	Asn	Asx	Glu	Leu	Trp	Ala	725	730	735	
	Asn	Asp	Ala	Arg	Glu	Asn	Thr	Asn	Thr	His	Glu	Asp	Ile	Ser	Lys	Glu	740	745	750	
10	Thr	Thr	Glu	Ser	Ser	Glu	Gln	Glu	Asn	Cys	Glu	Ser	Glu	Gln	Ile	Asp	755	760	765	
	Asn	Thr	Tyr	Pro	Glu	Thr	Pro	Leu	Gly	Tyr	Ser	Thr	Arg	Ala	Asn	Asp	770	775	780	
15	Ser	Pro	Glu	Cys	Ile	Ala	Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser	Glu	785	790	795	800
	Gln	Ile	Asp	Asn	Pro	Arg	Thr	Glu	Ile	Asn	Leu	Ile	Asn	Glu	Ala	Arg	805	810	815	
20	Asn	Ala	Tyr	Glu	Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser	Glu	Gln	Ile	820	825	830	
25	Asp	Asn	Pro	Arg	Thr	Glu	Ile	Asn	Leu	Ile	Asn	Glu	Ala	Arg	Asn	Ala	835	840	845	
	Tyr	Asp	Leu	Ala	Gln	Gln	Gln	Asp	Gln	His	Ser	Glu	Gln	Ile	Asp	Asn	850	855	860	
30	Pro	Arg	Thr	Glu	Ile	Asn	Leu	Ile	Asn	Glu	Ala	Arg	Asn	Ala	Gly	Ala	865	870	875	880
	Cys	Gly	Cys	Thr	Cys	Ala	Ala	Cys	Ala	Gly	Cys	Ala	Cys	Thr	Ala	Ala	885	890	895	
35	Thr	Ala	Cys	Gly	Ser	Glu	Gln	Ile	Asp	Asn	Asp	Asn	Ala	Leu	Ile	Asn	900	905	910	
40	Glu	Ala	Arg	Asp	Asx	Leu	Glu	Cys	Cys	Ala	Ala	Gly	Cys	Thr	Gly	Ala	915	920	925	
	Thr	Ala	Thr	Cys	Ala	Cys	Thr	Ala	Cys	Cys	Ser	Glu	Gln	Ile	Asp	Asn	930	935	940	
45	Asp	Asn	Ala	Leu	Ile	Asn	Glu	Ala	Arg	Asp	Asx	Leu	Glu	Thr	Cys	Ala	945	950	955	960
	Ala	Thr	Gly	Cys	Cys	Thr	Thr	Thr	Gly	Ala	Thr	Gly	Gly	Thr	Cys	Ser	965	970	975	
50	Glu	Gln	Ile	Asp	Asn	Asp	Asn	Ala	Leu	Ile	Asn	Glu	Ala	Arg	Asp	Asx	980	985	990	
55	Leu	Glu	Thr	Gly	Thr	Ala	Thr	Gly	Cys	Cys	Gly	Cys	Thr	Ala	Cys	Thr	995	1000	1005	

	Cys Gly Cys Ala Gly Cys Thr Ser Glu Gln Ile Asp Asn Asp Asn Ala	
	1010	1020
5	Leu Ile Asn Glu Ala Arg Asp Asx Leu Glu Asn Xaa Ala Xaa Xaa Tyr	
	1025	1035
	Ser Xaa Ile Gly Gly Gly Xaa Asn Ser Glu Gln Ile Asp Asn Pro Arg	
	1045	1055
10	Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr	
	1060	1070
	Ala Thr Pro Ser Ile Thr Ile Asn Ser Gln Ala Asp Ile Ser Glu Gln	
	1075	1085
15	Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn	
	1090	1100
20	Ala Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Val Pro Tyr Ser Val	
	1105	1115
	Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser	
	1125	1135
25	Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala	
	1140	1150
	Arg Asn Ala Gly Lys Ile Thr Lys Asn Ala Ala Arg Gln Glu Asn Gly	
	1155	1165
30	Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu	
	1170	1180
35	Ala Arg Asn Ala Val Ile Gly Asp Leu Gly Arg Lys Val Ser Glu Gln	
	1185	1195
	Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn	
	1205	1215
40	Ala Ala Leu Glu Xaa Asn Val Glu Glu Gly Leu Ser Glu Gln Ile Asp	
	1220	1230
	Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa	
	1235	1245
45	Ala Asn Tyr Ala Thr Pro Ser Ile Thr Ile Asn Ala Leu Glu Ser Asn	
	1250	1260
50	Val Glu Glu Gly Leu Xaa Xaa Leu Ser Ser Glu Gln Ile Asp Asn Pro	
	1265	1275
	Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn	
	1285	1295
55	Tyr Ala Thr Pro Ser Ile Thr Ile Asn Ser Ala Leu Glu Phe Asn Gly	
	1300	1310

Glu Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn
 1315 1320 1325
 Glu Ala Arg Asn Ala Ser Ile Thr Asp Leu Gly Xaa Lys Val Ser Glu
 5 1330 1335 1340
 Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg
 1345 1350 1355 1360
 10 Asn Ala Xaa Ala Asn Tyr Ala Thr Pro Ser Ile Thr Ile Asn Ser Ile
 1365 1370 1375
 Thr Asp Leu Gly Thr Ile Val Asp Gly Phe Xaa Xaa Xaa Ser Glu Gln
 15 1380 1385 1390
 Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn
 1395 1400 1405
 20 Ala Xaa Ala Asn Tyr Ala Thr Pro Ser Ile Thr Ile Asn Ser Ser Ile
 1410 1415 1420
 Thr Asp Leu Gly Thr Ile Val Asp Ser Glu Gln Ile Asp Asn Pro Arg
 1425 1430 1435 1440
 25 Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Val Asp Ala Leu
 1445 1450 1455
 Xaa Thr Lys Val Asn Ala Leu Asp Xaa Lys Val Asn Ser Asp Xaa Thr
 30 1460 1465 1470
 Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu
 1475 1480 1485
 35 Ala Arg Asn Ala Xaa Ala Asn Tyr Ala Thr Pro Ser Ile Thr Ile Asn
 1490 1495 1500
 Ser Leu Leu Ala Glu Gln Gln Leu Asn Gly Lys Thr Leu Thr Pro Val
 1505 1510 1515 1520
 40 Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu
 1525 1530 1535
 Ala Arg Asn Ala Ala Lys His Asp Ala Ala Ser Thr Glu Lys Gly Lys
 45 1540 1545 1550
 Met Asp Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
 1555 1560 1565
 Asn Glu Ala Arg Asn Ala Ala Leu Glu Ser Asn Val Glu Glu Gly Leu
 50 1570 1575 1580
 Leu Asp Leu Ser Gly Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile
 1585 1590 1595 1600
 55 Asn Leu Ile Asn Glu Ala Arg Asn Ala Asn Gln Asn Thr Leu Ile Glu
 1605 1610 1615

Lys Thr Ala Asn Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile
 1620 1625 1630
 Asn Leu Ile Asn Glu Ala Arg Asn Ala Ile Asp Lys Asn Glu Tyr Ser
 1635 1640 1645
 Ile Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
 1650 1655 1660
 Asn Glu Ala Arg Asn Ala Ser Ile Thr Asp Leu Gly Thr Lys Ser Glu
 1665 1670 1675 1680
 Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg
 1685 1690 1695
 Asn Ala Asn Gln Asn Thr Leu Ile Glu Lys Ser Glu Gln Ile Asp Asn
 1700 1705 1710
 Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Leu
 1715 1720 1725
 His Glu Gln Gln Leu Glu Thr Leu Thr Lys Ser Glu Gln Ile Asp Asn
 1730 1735 1740
 Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Asn Ser
 1745 1750 1755 1760
 Ser Asp Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
 1765 1770 1775
 Asn Glu Ala Arg Asn Ala Asn Lys Ala Asp Ala Asp Ala Ser Phe Glu
 1780 1785 1790
 Thr Leu Thr Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn
 1795 1800 1805
 Leu Ile Asn Glu Ala Arg Asn Ala Phe Ala Ala Thr Ala Ile Ala Lys
 1810 1815 1820
 Asp Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
 1825 1830 1835 1840
 Asn Glu Ala Arg Asn Ala Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile
 1845 1850 1855
 Ala Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
 1860 1865 1870
 Asn Glu Ala Arg Asn Ala Arg Leu Leu Asp Gln Lys Ser Glu Gln Ile
 1875 1880 1885
 Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
 1890 1895 1900
 Ala Ala Thr Ala Asp Ala Ile Thr Lys Asn Gly Xaa Ser Glu Gln Ile
 1905 1910 1915 1920

	Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala	
	1925	1930 1935
5	Ala Lys Ala Xaa Ala Ala Asn Xaa Asp Arg Ser Glu Gln Ile Asp Asn	
	1940	1945 1950
	Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala	
	1955	1960 1965
10	Asn Tyr Ala Thr Pro Ser Ile Thr Ile Asn Ser Asn Gln Ala Asp Ile	
	1970	1975 1980
	Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu Leu	
	1985	1990 1995 2000
15	Gln Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn	
	2005	2010 2015
	Glu Ala Arg Asn Ala Asn Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn	
20	2020	2025 2030
	Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln Ser Glu Gln Ile Asp Asn	
	2035	2040 2045
25	Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Tyr Asn	
	2050	2055 2060
	Glu Arg Gln Thr Glu Ala Ile Asp Ala Leu Asn Ser Glu Gln Ile Asp	
30	2065	2070 2075 2080
	Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ile	
	2085	2090 2095
35	Leu Gly Asp Thr Ala Ile Val Ser Asn Ser Gln Asp Ser Glu Gln Ile	
	2100	2105 2110
	Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala	
	2115	2120 2125
40	Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Gly	
	2130	2135 2140
	Arg Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn	
45	2145	2150 2155 2160
	Glu Ala Arg Asn Ala Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu	
	2165	2170 2175
	Glu Leu Ser Gly Arg Thr Ile Asp Gln Arg Ser Glu Gln Ile Asp Asn	
50	2180	2185 2190
	Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Asn Gln	
	2195	2200 2205
55	Ala His Ile Ala Asn Asn Ile Asn Xaa Ile Tyr Glu Leu Ala Gln Gln	
	2210	2215 2220

Gln Asp Gln Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn
 2225 2230 2235 2240
 5 Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr Ala Thr Pro Ser
 2245 2250 2255
 Ile Thr Ile Asn Asn Gln Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile
 2260 2265 2270
 10 Gln Asp Leu Ala Ala Tyr Asn Glu Leu Gln Ser Glu Gln Ile Asp Asn
 2275 2280 2285
 Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Thr
 2290 2295 2300
 15 His Asp Tyr Asn Glu Arg Gln Thr Glu Ala Ser Glu Gln Ile Asp Asn
 2305 2310 2315 2320
 Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Lys Ala
 2325 2330 2335
 20 Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Ser Glu Gln Ile Asp Asn
 2340 2345 2350
 Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Met Ile
 2355 2360 2365
 Leu Gly Asp Thr Ala Ile Val Ser Asn Ser Gln Asp Asn Lys Thr Gln
 2370 2375 2380
 30 Leu Lys Phe Tyr Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile
 2385 2390 2395 2400
 Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Gly Asp Thr Ile Ile Pro
 2405 2410 2415
 35 Leu Asp Asp Asp Xaa Xaa Pro Ser Glu Gln Ile Asp Asn Pro Arg Thr
 2420 2425 2430
 Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr Ala
 2435 2440 2445
 Thr Pro Ser Ile Thr Ile Asn Ser Leu Leu His Glu Gln Gln Leu Xaa
 2450 2455 2460
 45 Gly Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
 2465 2470 2475 2480
 Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr Ala Thr Pro Ser Ile Thr
 2485 2490 2495
 50 Ile Asn Ile Phe Phe Asn Xaa Gly Ser Glu Gln Ile Asp Asn Pro Arg
 2500 2505 2510
 Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr
 2515 2520 2525

Ala Thr Pro Ser Ile Thr Ile Asn Asn Asn Ile Asn Asn Ile Tyr Glu
2530 2535 2540

5 Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ser
2545 2550 2555 2560

Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala
2565 2570 2575

10 Arg Asn Ala Gly Gly Thr Gly Cys Ala Gly Gly Thr Cys Ala Gly Ala
2580 2585 2590

Thr Cys Ala Gly Thr Gly Ala Cys Ser Glu Gln Ile Asp Asn Asp Asn
2595 2600 2605

15 Ala Leu Ile Asn Glu Ala Arg Asp Asx Leu Glu Gly Cys Cys Ala Cys
2610 2615 2620

20 Cys Ala Ala Cys Cys Ala Ala Gly Cys Thr Gly Ala Cys Ser Glu Gln
2625 2630 2635 2640

Ile Asp Asn Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp Asx Leu Glu
2645 2650 2655

25 Ala Gly Cys Gly Gly Thr Cys Gly Cys Cys Thr Gly Cys Thr Thr Gly
2660 2665 2670

Ala Thr Cys Ala Gly Ser Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile
2675 2680 2685

30 Asn Glu Ala Arg Asp Asx Leu Glu Cys Thr Gly Ala Thr Cys Ala Ala
2690 2695 2700

Gly Cys Ala Gly Gly Cys Gly Ala Cys Cys Gly Cys Thr Ser Glu Gln
2705 2710 2715 2720

Ile Asp Asn Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp Asx Leu Glu
2725 2730 2735

40 Cys Ala Ala Gly Ala Thr Cys Thr Gly Gly Cys Cys Gly Cys Thr Thr
2740 2745 2750

Ala Cys Ala Ala Ser Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile Asn
2755 2760 2765

45 Glu Ala Arg Asp Asx Leu Glu Thr Thr Gly Thr Ala Ala Gly Cys Gly
2770 2775 2780

Gly Cys Cys Ala Gly Ala Thr Cys Thr Thr Gly Ser Glu Gln Ile Asp
2785 2790 2795 2800

50 Asn Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp Asx Leu Glu Thr Gly
2805 2810 2815

55 Cys Ala Thr Gly Ala Gly Cys Cys Gly Cys Ala Ala Ala Cys Cys Cys
2820 2825 2830

Ser Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp
 2835 2840 2845
 5 Asx Leu Glu Leu Leu Ala Glu Gln Gln Leu Asn Gly Ser Glu Gln Ile
 2850 2855 2860
 Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
 2865 2870 2875 2880
 10 Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Ser Glu Gln Ile Asp Asn
 2885 2890 2895
 Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Leu
 2900 2905 2910
 15 Glu Ser Asn Val Glu Glu Gly Leu Leu Asp Leu Ser Ser Glu Gln Ile
 2915 2920 2925
 Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
 2930 2935 2940
 20 Asn Ala Lys Ala Ser Ala Ala Asn Thr Asp Arg Ser Glu Gln Ile Asp
 2945 2950 2955 2960
 25 Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala
 2965 2970 2975
 Ala Thr Ala Ala Asp Ala Ile Thr Lys Asn Gly Asn Ser Glu Gln Ile
 2980 2985 2990
 30 Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
 2995 3000 3005
 35 Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Ser
 3010 3015 3020
 Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala
 3025 3030 3035 3040
 40 Arg Asn Ala Val Asp Ala Leu Xaa Thr Lys Val Asn Ala Leu Asp Xaa
 3045 3050 3055
 Lys Val Asn Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu
 3060 3065 3070
 45 Ile Asn Glu Ala Arg Asn Ala Xaa Ala Asn Tyr Ala Thr Pro Ser Ile
 3075 3080 3085
 Thr Ile Asn Ser Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Val Pro
 3090 3095 3100
 50 Tyr Ser Val Gly Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly
 3105 3110 3115 3120
 55 Ser Lys Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
 3125 3130 3135

Asn Glu Ala Arg Asn Ala Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp
 3140 3145 3150

5 Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu
 3155 3160 3165

Ala Arg Asn Ala Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn Ser Glu
 3170 3175 3180

10 Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg
 3185 3190 3195 3200

Asn Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Ser Glu Gln Ile
 3205 3210 3215

15 Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
 3220 3225 3230

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Ser Glu Gln Ile Asp Asn
 20 3235 3240 3245

Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Gln
 3250 3255 3260

25 Gln Gln Asp Gln His Ser Ser Asp Ser Glu Gln Ile Asp Asn Pro Arg
 3265 3270 3275 3280

Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Gln Asp Gln His
 3285 3290 3295

30 Ser Ser Asp Ile Lys Thr Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu
 3300 3305 3310

Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala His Ser Ser Asp Ile Lys
 35 3315 3320 3325

Thr Leu Lys Asn Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn
 3330 3335 3340

40 Leu Ile Asn Glu Ala Arg Asn Ala Asp Ile Lys Thr Leu Lys Asn Asn
 3345 3350 3355 3360

Val Glu Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
 45 3365 3370 3375

Asn Glu Ala Arg Asn Ala Thr Leu Lys Asn Asn Val Glu Glu Gly Leu
 3380 3385 3390

Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu
 50 3395 3400 3405

Ala Arg Asn Ala Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg Ser Glu
 3410 3415 3420

55 Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg
 3425 3430 3435 3440

Asn Ala Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Ser Glu Gln Ile
 3445 3450 3455

5 Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala
 3460 3465 3470

Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln Ser Glu Gln Ile Asp Asn
 3475 3480 3485

10 Pro Arg Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ala Lys
 3490 3495 3500

Asn Gln Ala Asp Ile Ala Gln Asn Ser Glu Gln Ile Asp Asn Pro Arg
 3505 3510 3515 3520

15 Thr Glu Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Ile Ala Gln Asn
 3525 3530 3535

Gln Thr Asp Ile Gln Asp Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu
 3540 3545 3550

20 Ile Asn Leu Ile Asn Glu Ala Arg Asn Ala Asp Ile Gln Asp Leu Ala
 3555 3560 3565

25 Ala Tyr Asn Glu Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn
 3570 3575 3580

Leu Ile Asn Glu Ala Arg Asn Ala Cys Gly Gly Gly Ala Thr Cys Cys
 3585 3590 3595 3600

30 Gly Thr Gly Ala Ala Gly Ala Ala Ala Ala Ala Thr Gly Cys Cys Gly
 3605 3610 3615

Cys Ala Gly Gly Thr Ser Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile
 3620 3625 3630

35 Asn Glu Ala Arg Asp Asx Leu Glu Cys Gly Gly Gly Ala Thr Cys Cys
 3635 3640 3645

40 Cys Gly Thr Cys Gly Cys Ala Ala Gly Cys Cys Gly Ala Thr Thr Gly
 3650 3655 3660

Ser Glu Gln Ile Asp Asn Asp Asn Ala Leu Ile Asn Glu Ala Arg Asp
 3665 3670 3675 3680

45 Asx Leu Glu Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp Ile Asp Asn
 3685 3690 3695

Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser
 3700 3705 3710

Ser Asp Ile Lys Thr Leu Lys Asn Asn Val Glu Glu Gly Leu Leu Asp
 3715 3720 3725

55 Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln
 3730 3735 3740

Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr
3745 3750 3755 3760

Asn Glu Ser Glu Gln Ile Asp Asn Pro Arg Thr Glu Ile Asn Leu Ile
3765 3770 3775

Asn Glu Ala Arg Asn Ala Ala Trp Glx Xaa Asp Cys
3780 3785

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Ala Ala Thr Ala Ala Asp Ala Ile Thr Lys Asn Gly Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ser Ile Thr Asp Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5..13
- (D) OTHER INFORMATION: /note= "X = any"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Val Asp Ala Leu Xaa Thr Lys Val Asn Ala Leu Asp Xaa Lys Val Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ala Ala Gln Ala Ala Leu Ser Gly Leu Phe Val Pro Tyr Ser Val Gly
1 5 10 15
Lys Phe Asn Ala Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys
20 25 30

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Asn Asn Ile Tyr Glu Leu Ala Gln Gln Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Ala Gln Gln Gln Asp Gln His Ser Ser Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Gln Asp Gln His Ser Ser Asp Ile Lys Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

His Ser Ser Asp Ile Lys Thr Leu Lys Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Asp Ile Lys Thr Leu Lys Asn Asn Val Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Thr Leu Lys Asn Asn Val Glu Glu Gly Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Glu Glu Gly Leu Leu Asp Leu Ser Gly Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Leu Ser Gly Arg Leu Ile Asp Gln Lys Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Ala Lys Asn Gln Ala Asp Ile Ala Gln Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CGGGATCCGT GAAGAAAAAT GCCGCAGGT

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CGGGATCCCG TCGCAAGCCG ATTG

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp Ile Asp Asn Asn Ile Asn
 1 5 10 15

Asn Ile Tyr Glu Leu Ala Gln Gln Gln Asp Gln His Ser Ser Asp Ile
 20 25 30

Lys Thr Leu Lys Asn Asn Val Glu Gly Leu Leu Asp Leu Ser Gly
 35 40 45

Arg Leu Ile Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln Ala Asp Ile
 50 55 60

Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr Asn Glu
 65 70 75

CLAIMS

1. An isolated peptide of about 7 to about 60 amino acids comprising the amino acid sequence AQQQDQH (SEQ ID NO:17).
- 5 2. The isolated peptide of claim 1, wherein said peptide is about 10 amino acids in length.
3. The isolated peptide of claim 1, wherein said peptide is about 20 amino acids in length.
- 10 4. The isolated peptide of claim 1, wherein said peptide is about 30 amino acids in length.
5. The isolated peptide of claim 1, wherein said peptide is about 40 amino acids in length.
6. The isolated peptide of claim 1, wherein said peptide is about 50 amino acids in length.
- 15 7. The isolated peptide of claim 1, wherein said peptide is about 60 amino acids in length.
8. The isolated peptide of claim 1, wherein said peptide is at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).

20

9. An antigenic composition comprising (a) an isolated peptide of about 7 to about 60 amino acids comprising the amino acid sequence AQQQDQH (SEQ ID NO:17) and (b) a pharmaceutically acceptable buffer or diluent.
- 5 10. The antigenic composition of claim 9, wherein said antigenic composition further comprises a carrier conjugated to said peptide.
11. The antigenic composition of claim 10, wherein said carrier is KLH, diphtheria toxoid, tetanus toxoid or CRM₁₉₇.
- 10 12. The antigenic composition of claim 9, further comprising an adjuvant.
13. The antigenic composition of claim 12, wherein said adjuvant comprises a lipid.
- 15 14. The antigenic composition of claim 9 wherein said peptide is covalently linked to a second antigen.
15. The antigenic composition of claim 14, wherein said second antigen is a peptide antigen.
- 20 16. The antigenic composition of claim 14, wherein said second antigen is a non-peptide antigen.

17. The antigenic composition of claim 9, wherein said isolated peptide comprises at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).
- 5 18. A vaccine composition comprising an isolated peptide of about 7 to about 60 amino acids comprising the amino acid sequence AQQQDQH (SEQ ID NO:17) and a pharmaceutically acceptable buffer or diluent.
- 10 19. The vaccine composition of claim 18, wherein said isolated peptide is further defined as comprising at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).
- 15 20. A method for inducing an immune response in a mammal comprising the step of providing to said mammal an antigenic composition comprising (a) an isolated peptide of about 7 to about 60 amino acids comprising the amino acid sequence AQQQDQH (SEQ ID NO:17) and (b) a pharmaceutically acceptable buffer or diluent.
- 20 21. The method of claim 20, wherein said isolated peptide is further defined as comprising at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).
22. A nucleic acid encoding the UspA1 antigen (SEQ ID NO:1) of the *M. catarrhalis* isolate O35E.

23. A nucleic acid having the *uspA1* DNA sequence (SEQ ID NO:2) of the *M. catarrhalis* isolate O35E.
24. A nucleic acid encoding the UspA2 antigen (SEQ ID NO:3) of the *M. catarrhalis* isolate O35E.
25. A nucleic acid having the *uspA2* DNA sequence (SEQ ID NO:4) of the *M. catarrhalis* isolate O35E.
26. A nucleic acid encoding the UspA1 antigen (SEQ ID NO:5) of the *M. catarrhalis* isolate O46E.
27. A nucleic acid having the *uspA1* DNA sequence (SEQ ID NO:6) of the *M. catarrhalis* isolate O46E.
28. A nucleic acid encoding the UspA2 antigen (SEQ ID NO:7) of the *M. catarrhalis* isolate O46E.
29. A nucleic acid having the *uspA2* DNA sequence (SEQ ID NO:8) of the *M. catarrhalis* isolate O46E.
30. A nucleic acid encoding the UspA1 antigen (SEQ ID NO:9) of the *M. catarrhalis* isolate TTA24.

31. A nucleic acid having the *uspA1* DNA sequence (SEQ ID NO:10) of the *M. catarrhalis* isolate TTA24.

5 32. A nucleic acid encoding the UspA2 antigen (SEQ ID NO:11) of the *M. catarrhalis* isolate TTA24.

33. A nucleic acid having the *uspA2* DNA sequence (SEQ ID NO:12) of the *M. catarrhalis* isolate TTA24.

10

34. A nucleic acid encoding the UspA1 antigen (SEQ ID NO:13) of the *M. catarrhalis* isolate TTA37.

15

35. A nucleic acid having the *uspA1* DNA sequence (SEQ ID NO:14) of the *M. catarrhalis* isolate TTA37.

36. A nucleic acid encoding the UspA2 antigen (SEQ ID NO:15) of the *M. catarrhalis* isolate TTA37.

20

37. A nucleic acid having the *uspA2* DNA sequence (SEQ ID NO:16) of the *M. catarrhalis* isolate TTA37.

38. A method for diagnosing *M. catarrhalis* infection comprising the step of determining the presence, in a sample, of an *M. catarrhalis* amino acid sequence corresponding to residues of epitopic core sequences of said UspA1 or UspA2 antigen.

5 39. The method of claim 38, wherein said determining comprises PCR.

40. The method of claim 38, wherein said determining comprises immunologic reactivity of an antibody to an *M. catarrhalis* antigen.

10 41. A method for treating an individual having an *M. catarrhalis* infection comprising providing to said individual an isolated peptide of about 7 to about 60 amino acids comprising the amino acid sequence AQQQDQH (SEQ ID NO:17).

15 42. The isolated peptide of claim 41, wherein the said peptide comprises at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).

43. A method for preventing or limiting an *M. catarrhalis* infection comprising providing to a subject an antibody that reacts immunologically with an epitope formed by the amino acid sequence AQQQDQH (SEQ ID NO:17).

20 44. The method of claim 42, wherein said epitope is further defined as comprising at least about 16 consecutive residues of the amino acid sequence YELAQQQDQH (SEQ ID NO:18).

45. A method for screening a peptide for reactivity with an antibody that bind immunologically to UspA1 or UspA2 comprising the steps of:

- a) providing said peptide;
- b) contacting said peptide with said antibody; and
- 5 c) determining the binding of said antibody to said peptide.

46. The method of claim 45, wherein said antibody is 17C7, 45-2, 13-1, 29-31, 16A7, 17B1 or 5C12.

10 47. The method of claim 46, wherein said antibody is 17C7.

48. The method of claim 46, wherein said antibody is 45-2.

49. The method of claim 46, wherein said antibody is 13-1.

15

50. The method of claim 46, wherein said antibody is 29-31.

51. The method of claim 46, wherein said antibody is 16A7.

20 52. The method of claim 46, wherein said antibody is 5C12.

53. The method of claim 46, wherein said antibody is 17B1.

54. The method of claim 45, wherein said determining comprises an immunoassay selected from the group consisting of a western blot, an ELISA, and RIA and immunoaffinity separation.

55. A method for screening a UspA1 or UspA2 peptide for the ability to induce a protective immune response against *M. catarrhalis* comprising the steps of:

- a) providing said peptide;
- b) administering a peptide in a suitable form to an experimental animal;
- c) challenging said animal with *M. catarrhalis*; and
- d) assaying the infection of said animal with *M. catarrhalis*.

56. The method of claim 56, wherein said animal is a mouse, said challenging is a pulmonary challenge, and said assaying comprises assessing the degree of pulmonary clearance by said mouse.

57. The method of claim 56, wherein said UspA1 peptide encompasses about residues 582-604 (SEQ ID NO:1) of *M. catarrhalis* or the analogous position thereof when compared to *M. catarrhalis* strain O35E.

58. The method of claim 56, wherein said UspA2 peptide encompasses about residues 355-377 (SEQ ID NO:3) of *M. catarrhalis* or the analogous position thereof when compared to *M. catarrhalis* strain O35E.

59. The method of claim 57, wherein said UspA1 peptide includes about residues 452-642 (SEQ ID NO:1) of *M. catarrhalis* or the analogous positions thereof when compared to *M. catarrhalis* strain O35E.

5

60. The method of claim 58, wherein said UspA2 peptide includes about residues 242-415 (SEQ ID NO:3) of *M. catarrhalis*, or the analogous position thereof when compared to *M. catarrhalis* strain O35E.

- 10 61. An isolated peptide having at least about 7 consecutive amino acids from the UspA1 or UspA2 protein of *M. catarrhalis*, wherein said peptide includes residues located within the region defined by about residues 582-604 of said UspA1 protein (SEQ ID NO:1), or by about residues 355-377 of said UspA2 protein (SEQ ID NO:3), or the analogous positions thereof when compared to strain O35E.

15

62. The isolated peptide of claim 61, wherein said peptide is between 7 and 60 amino acids in length.

20

63. The isolated peptide of claim 61, wherein said peptide comprises non-UspA1 or non-UspA2 sequences.

64. The isolated peptide of claim 61, wherein said peptide comprises non-*M. catarrhalis* sequences.

65. An antigenic composition comprising

- 5 a) an isolated peptide having at least about 7 consecutive amino acids from the UspA1 or UspA2 protein of *M. catarrhalis*, wherein said amino acids include residues located within the region defined by about residues 582-604 of said UspA1 protein (SEQ ID NO:1), or by about residues 355-377 of said UspA2 protein (SEQ ID NO:3), or the analogous positions thereof when compared to strain O35E.
- b) a pharmaceutically acceptable buffer or diluent.

10 66. An antigenic composition comprising

- a) an isolated peptide of about 7 to about 60 amino acids comprising at least 7 consecutive residues of the amino acid sequence of UspA1 or UspA2 wherein said isolated peptide acts as a carrier covalently linked to a second antigen; and
- b) a pharmaceutically acceptable buffer or diluent.

15

67. The antigenic composition of claim 66, wherein said second antigen is a peptide antigen.

68. The antigenic composition of claim 66, wherein said second antigen is a non-peptide antigen.

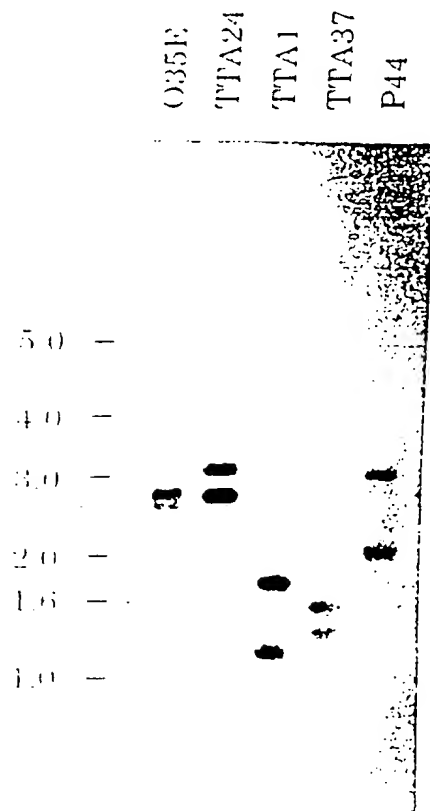


Fig. 1

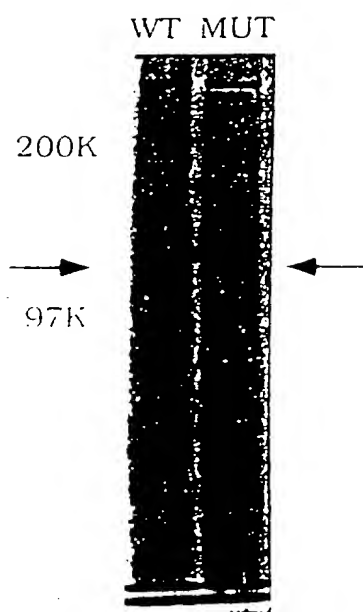


Fig. 2A

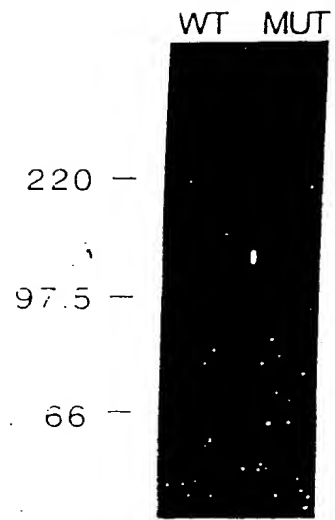


Fig. 2B

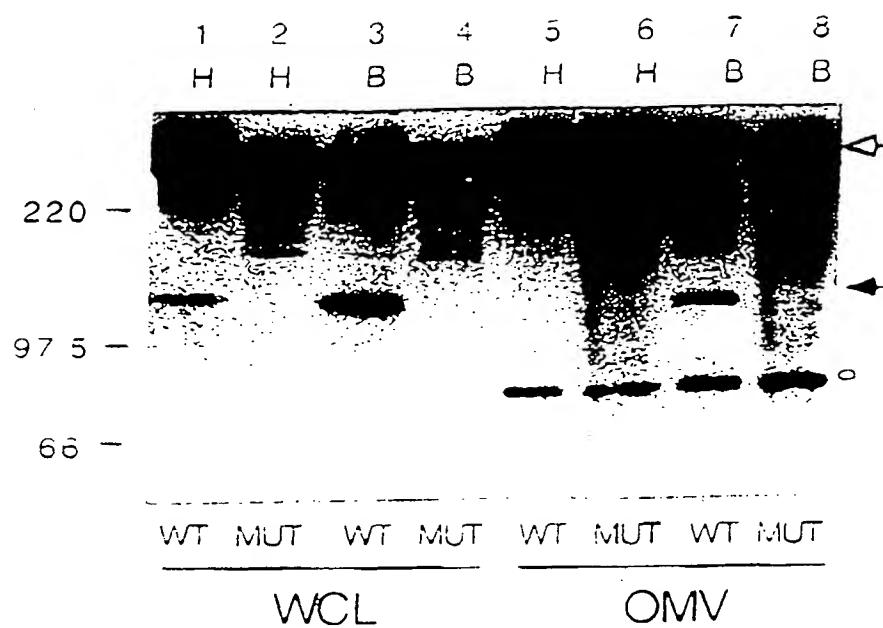


Fig. 2C

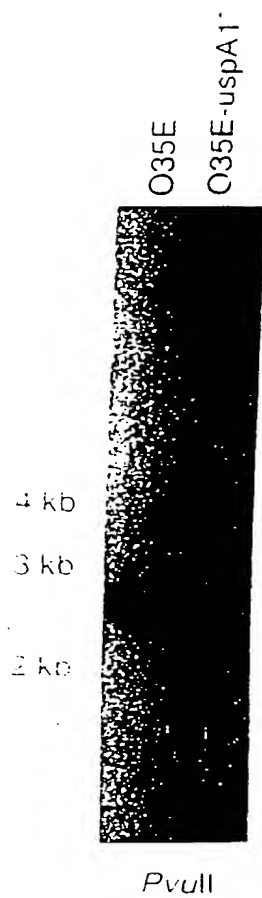


Fig. 3



Fig. 4

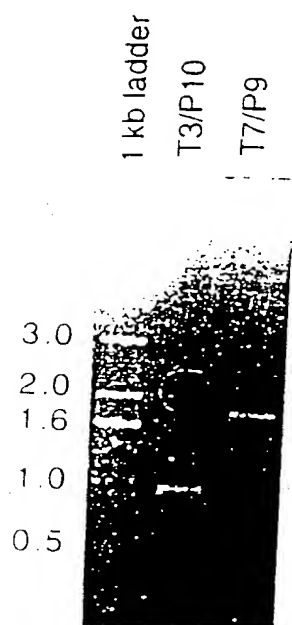


Fig. 5

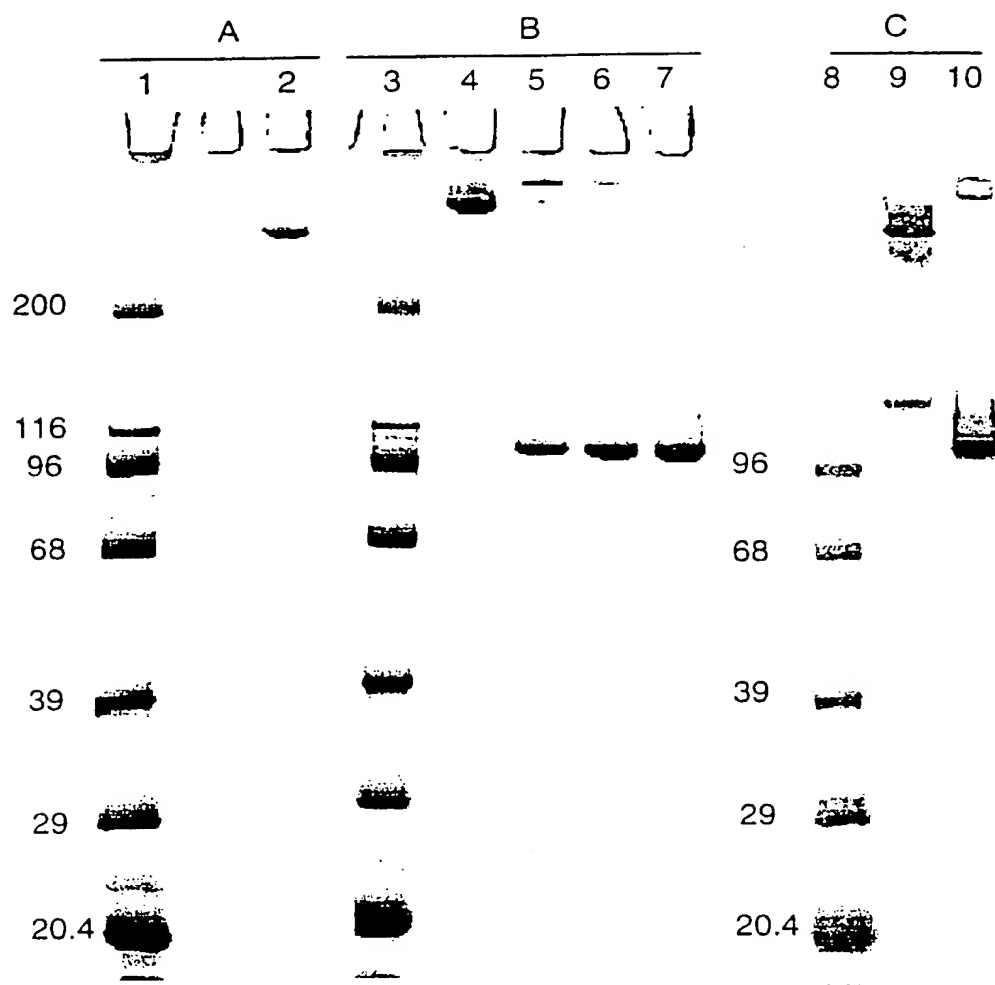


Fig 6

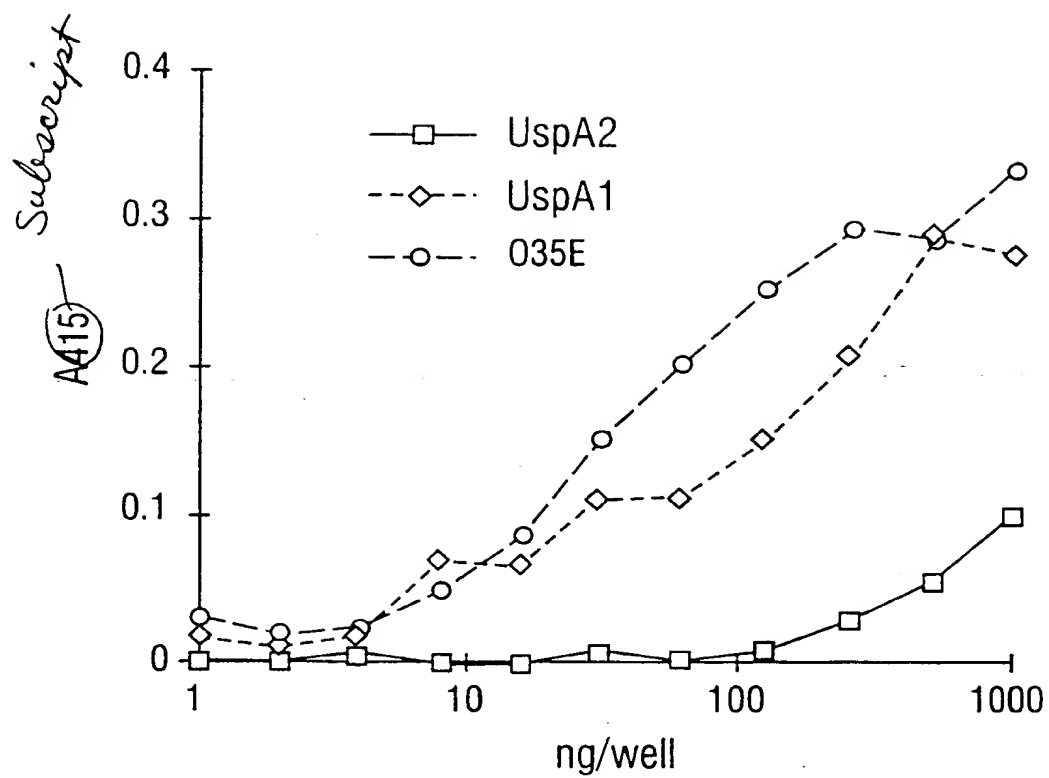


Fig. 7

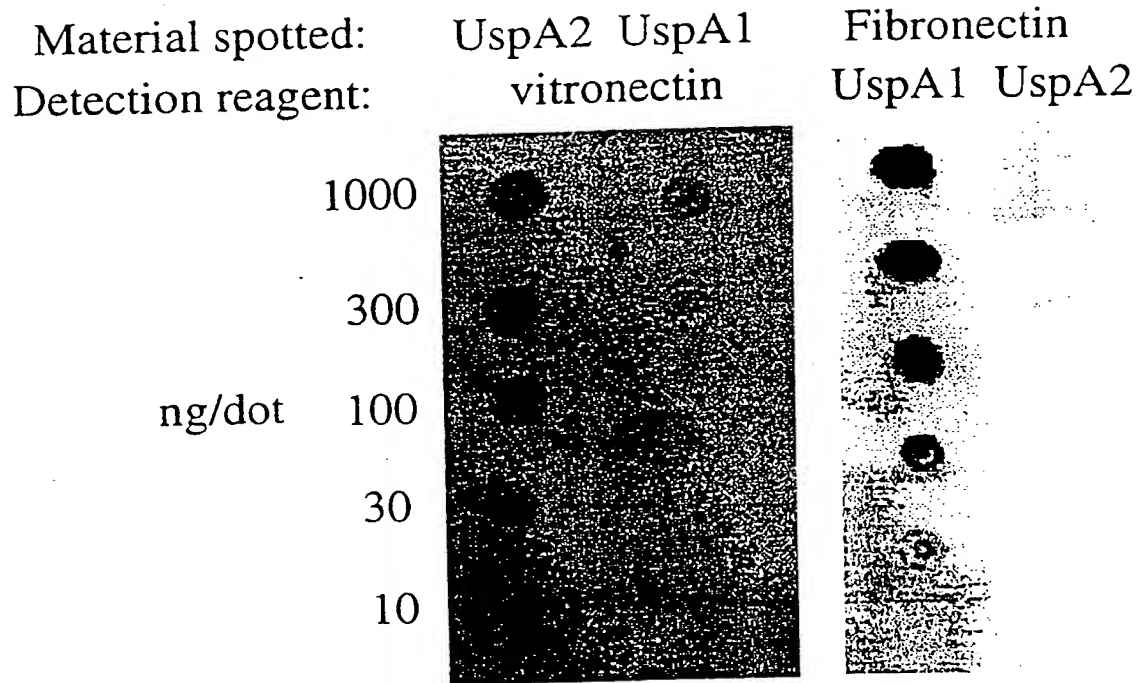


Fig. 8

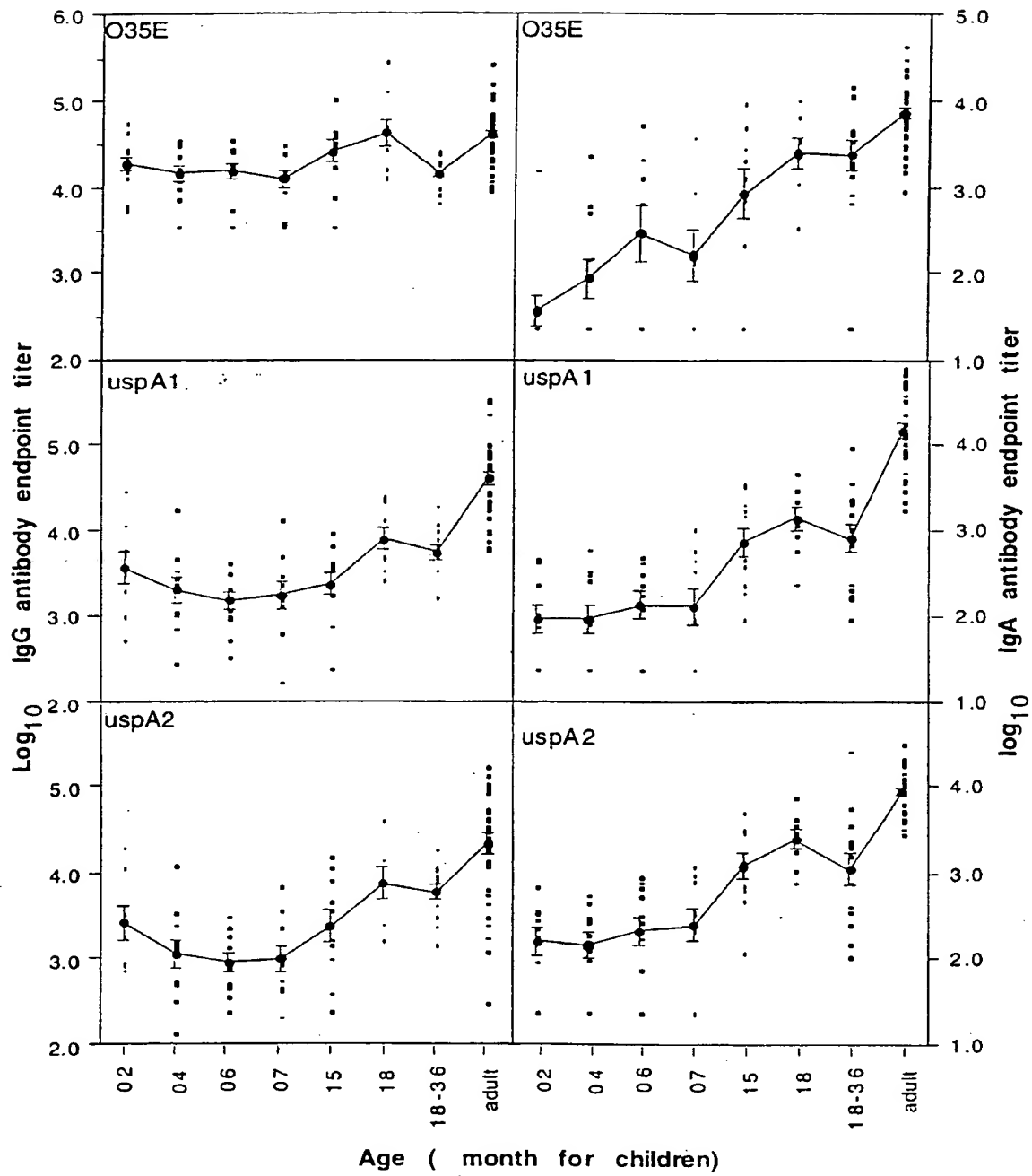


Fig. 9

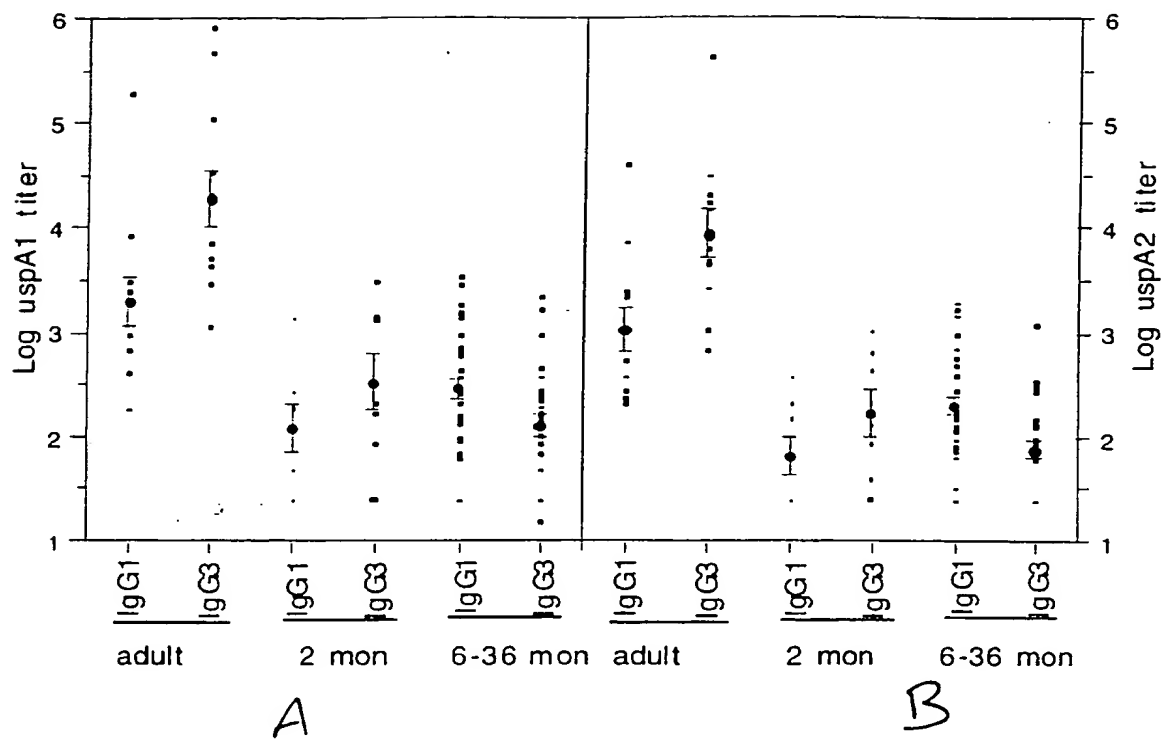


Fig. 10

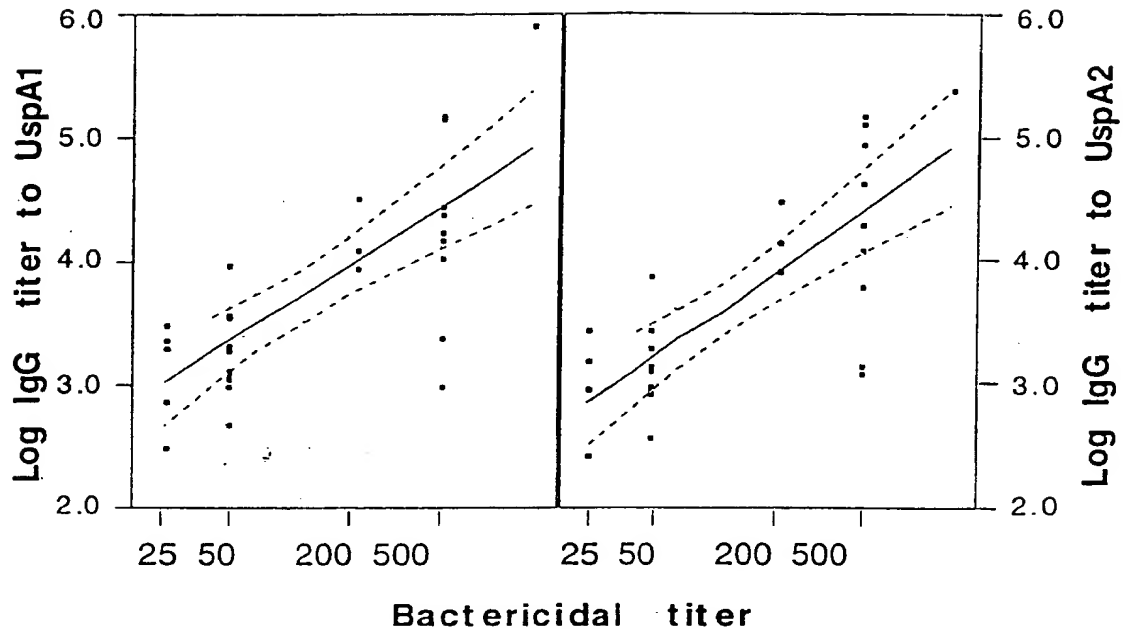


Fig. 11

MAB 17C7 EPI TOPE MAPPING

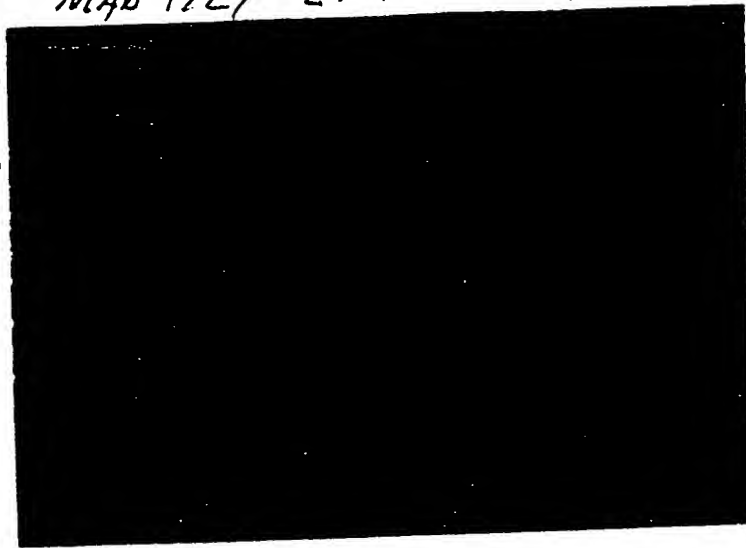


Fig. 12

1 10 20 30 40 50 60 70
 NH₂-SGRLDQKADIDNNINNIVELAQQQDQHSSDIKTLKNNYEEQLLDLSQRLIDQKADIAKNQADIAQNQTDIQDLAAYNE

(SEQ ID NO: 18)

λ ∅

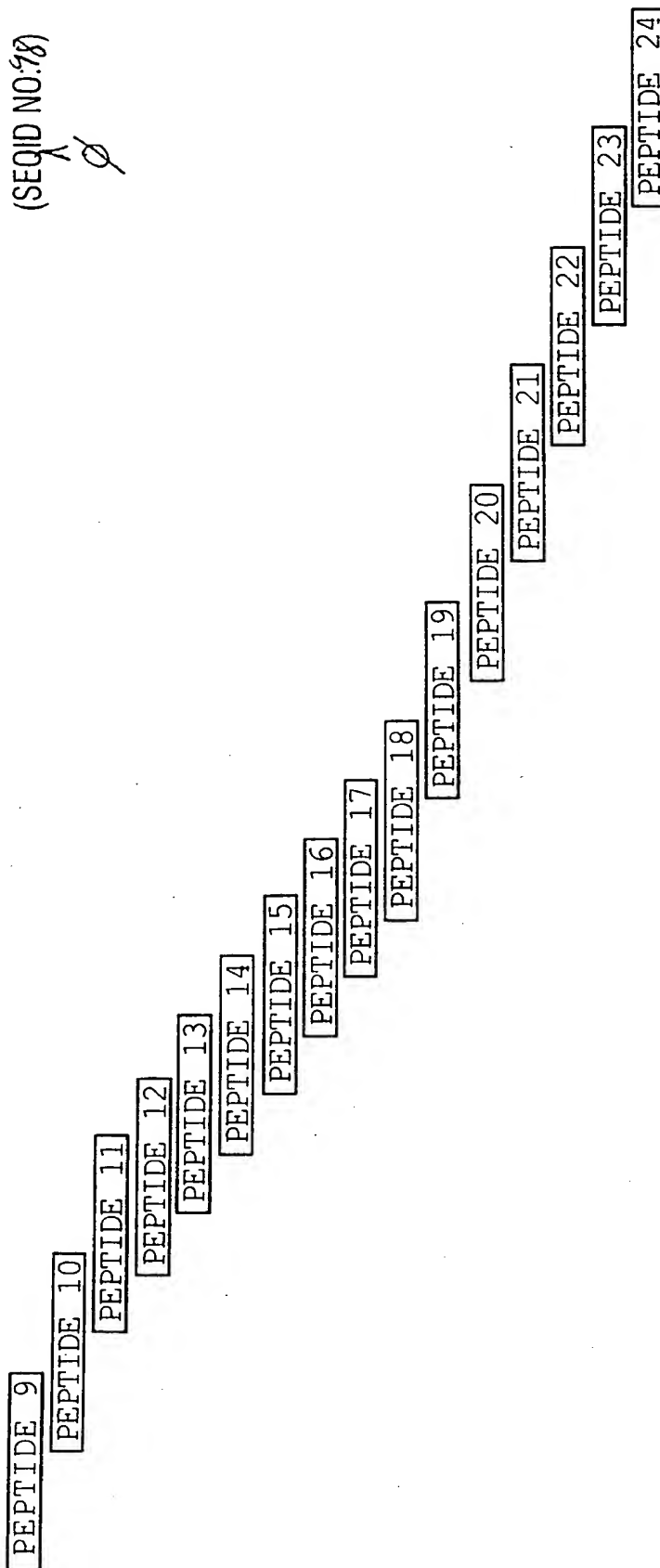


Fig. 13

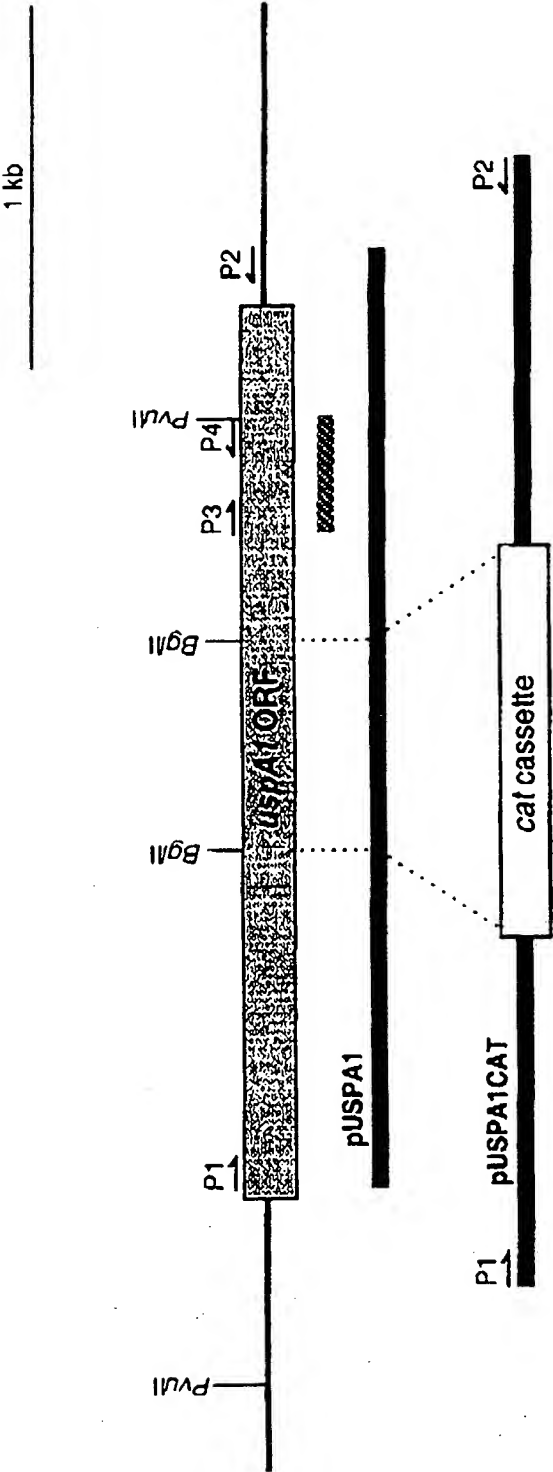


FIG. 14A

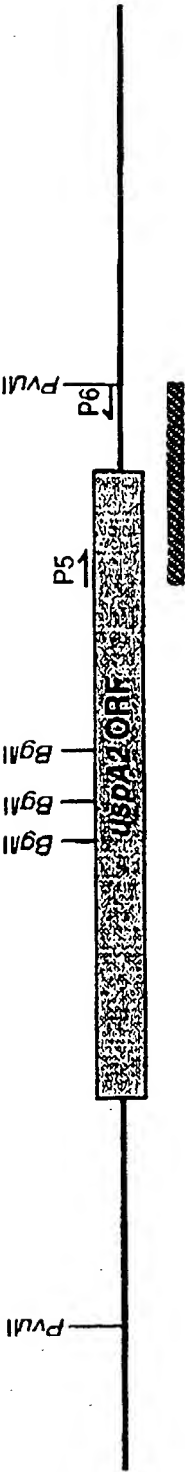


FIG. 14B

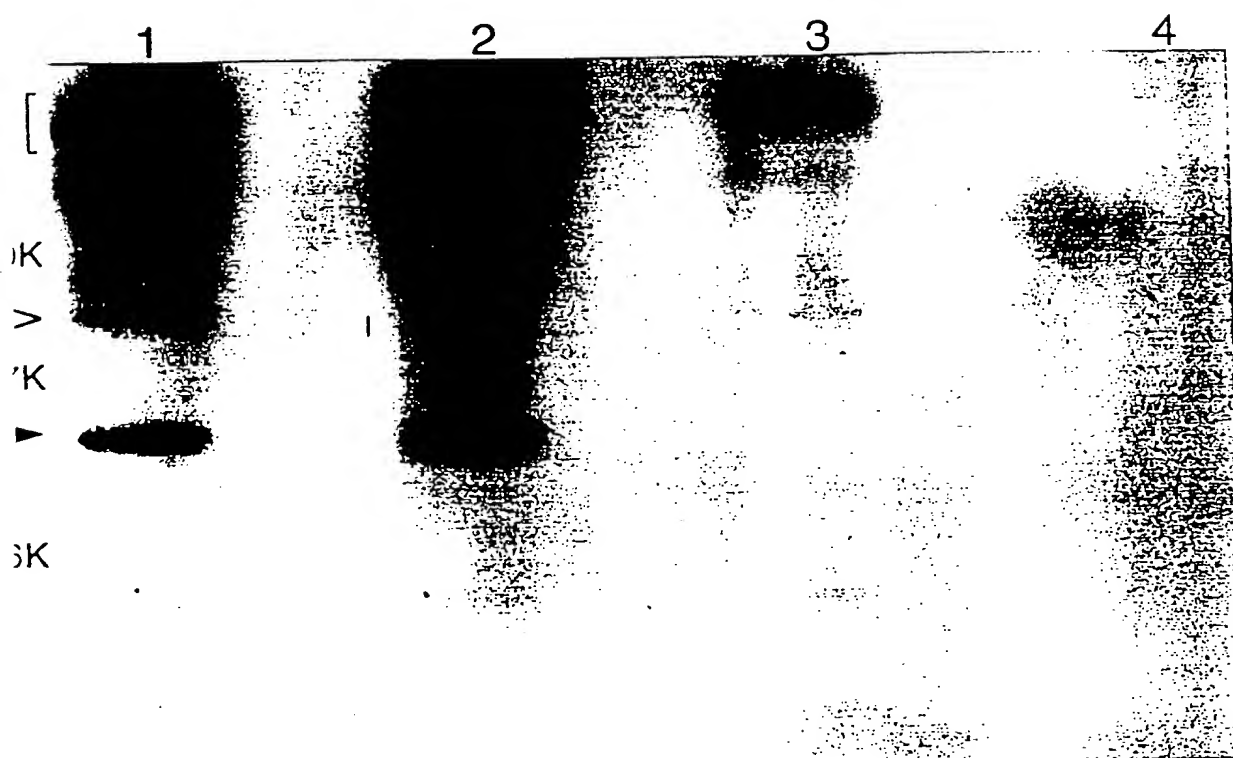
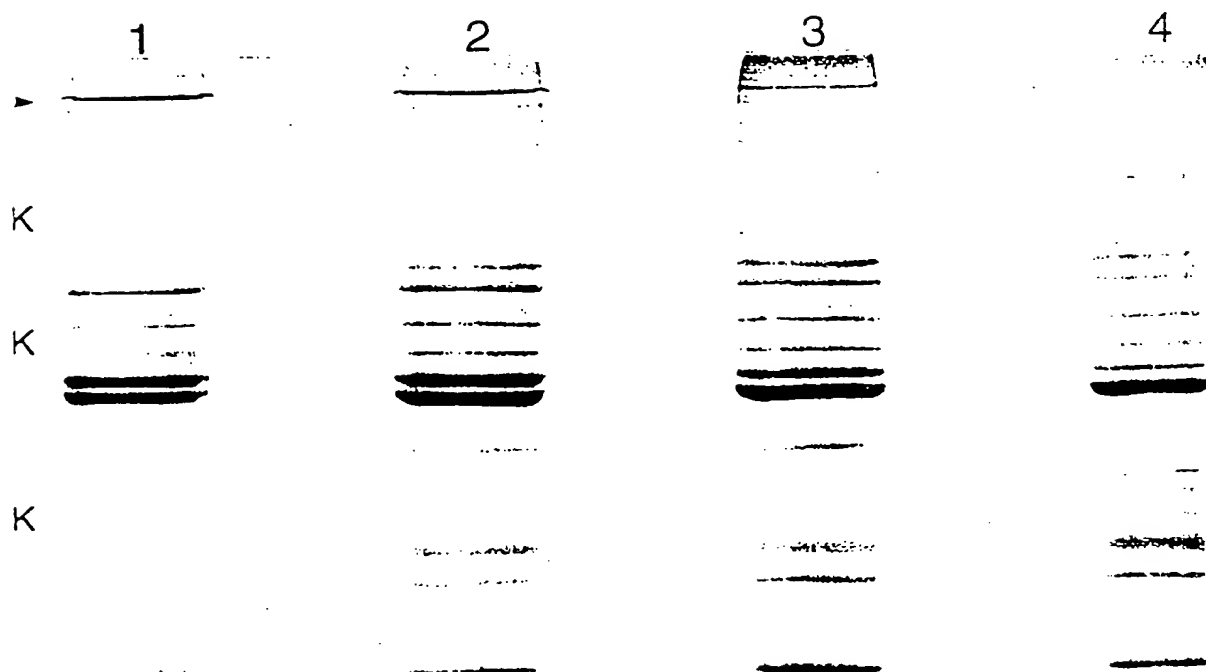


Fig. 15

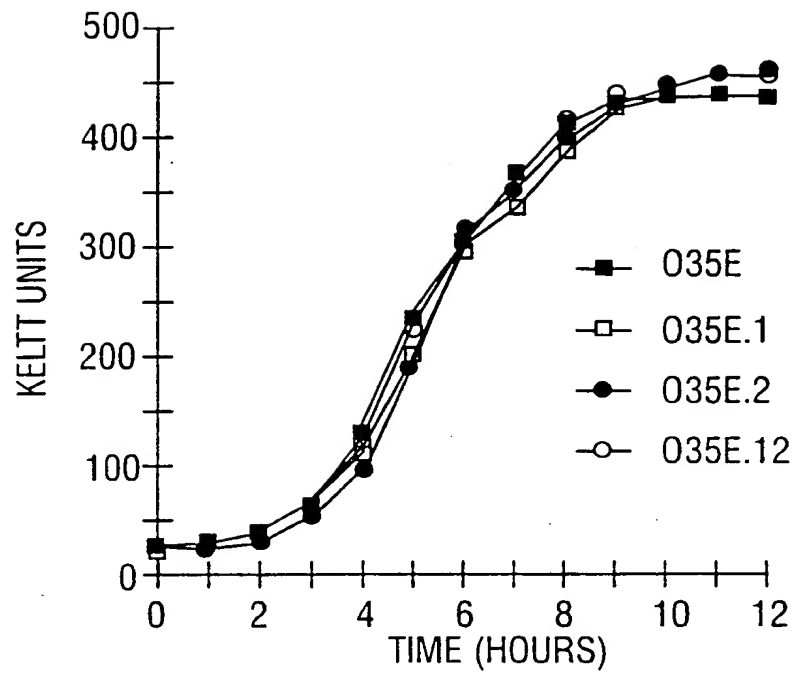


FIG. 18/6

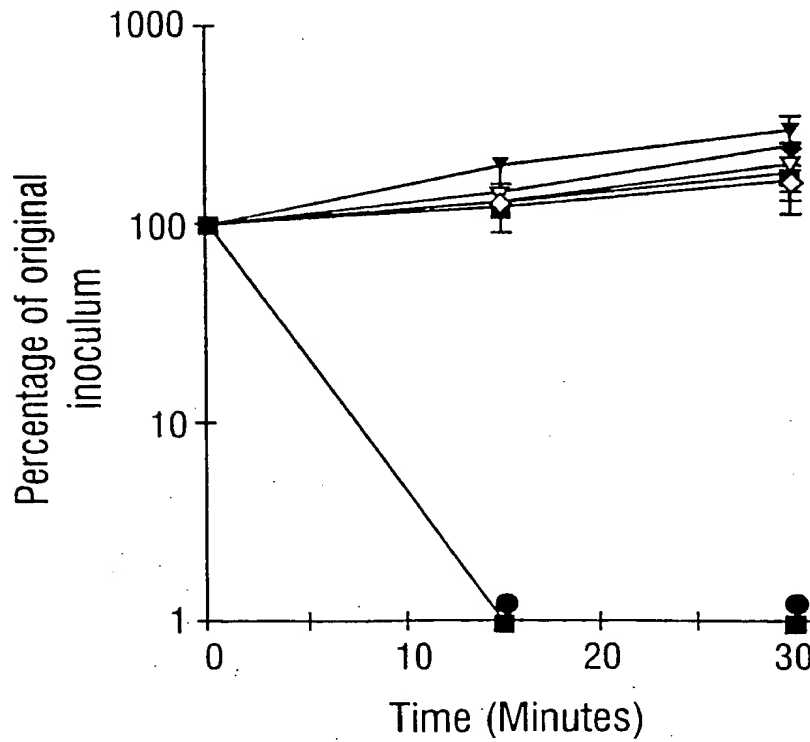


Fig. 16

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C07K 14/00	A2	(11) International Publication Number: WO 98/28333 (43) International Publication Date: 2 July 1998 (02.07.98)
<p>(21) International Application Number: PCT/US97/23930</p> <p>(22) International Filing Date: 19 December 1997 (19.12.97)</p> <p>(30) Priority Data: 60/033,598 20 December 1996 (20.12.96) US</p> <p>(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 60/033,598 (CIP) Filed on 20 December 1996 (20.12.96)</p> <p>(71) Applicant (for all designated States except US): THE BOARD OF REGENTS, THE UNIVERSITY OF TEXAS SYSTEM [US/US]; 201 West 7th Street, Austin, TX 78701 (US).</p> <p>(72) Inventors; and (75) Inventors/Applicants (for US only): HANSEN, Eric, J. [US/US]; 2404 Chamberlain Drive, Plano, TX 75023 (US). AEBI, Christoph [CH/US]; Gaselstrasse 165, CH-3144 Gasel (US). COPE, Leslie, D. [US/US]; 3244 North Galloway #118, Mesquite, TX 75150 (US). MACIVER, Isobel [GB/US]; Suite 254, 6721 Larmanda, Dallas, TX 75231 (US). FISKE, Michael, J. [US/US]; 167 Wood</p>		<p>Run, Rochester, NY 14612 (US). FREDENBURG, Ross [US/US]; 46 Nantucket Road, Rochester, NY 14626 (US).</p> <p>(74) Agent: HIGHLANDER, Steven, L.; Arnold, White & Durkee, P.O. Box 4433, Houston, TX 77210 (US).</p> <p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p>Published <i>Without international search report and to be republished upon receipt of that report.</i></p>
<p>(54) Title: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS</p>		
<p>(57) Abstract</p> <p>The present invention discloses the existence of two novel proteins UspA1 and UspA2, and their respective genes <i>uspA1</i> and <i>uspA2</i>. Each protein encompasses a region that is conserved between the two proteins and comprises an epitope that is recognized by MAb 17C7. One or more than one of these species may aggregate to form the very high molecular weight form (i.e. greater than 200 kDa) of the UspA antigen. Compositions and both diagnostic and therapeutic methods for the treatment and study of <i>M. catarrhalis</i> are disclosed.</p>		

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶: C07K 14/00	A2	(11) International Publication Number: WO 98/28333 (43) International Publication Date: 2 July 1998 (02.07.98)
(21) International Application Number: PCT/US97/23930 (22) International Filing Date: 19 December 1997 (19.12.97) (30) Priority Data: 60/033,598 20 December 1996 (20.12.96) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 60/033,598 (CIP) Filed on 20 December 1996 (20.12.96) (71) Applicant (for all designated States except US): THE BOARD OF REGENTS, THE UNIVERSITY OF TEXAS SYSTEM [US/US]; 201 West 7th Street, Austin, TX 78701 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): HANSEN, Eric, J. [US/US]; 2404 Chamberlain Drive, Plano, TX 75023 (US). AEBI, Christoph [CH/US]; Gaselstrasse 165, CH-3144 Gasel (US). COPE, Leslie, D. [US/US]; 3244 North Galloway #118, Mesquite, TX 75150 (US). MACIVER, Isobel [GB/US]; Suite 254, 6721 Larmanda, Dallas, TX 75231 (US). FISKE, Michael, J. [US/US]; 167 Wood		Run, Rochester, NY 14612 (US). FREDENBURG, Ross [US/US]; 46 Nantucket Road, Rochester, NY 14626 (US). (74) Agent: HIGHLANDER, Steven, L.; Arnold, White & Durkee, P.O. Box 4433, Houston, TX 77210 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published Without international search report and to be republished upon receipt of that report.
(54) Title: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS (57) Abstract <p>The present invention discloses the existence of two novel proteins UspA1 and UspA2, and their respective genes <i>uspA1</i> and <i>uspA2</i>. Each protein encompasses a region that is conserved between the two proteins and comprises an epitope that is recognized by MAb 17C7. One or more than one of these species may aggregate to form the very high molecular weight form (i.e. greater than 200 kDa) of the UspA antigen. Compositions and both diagnostic and therapeutic methods for the treatment and study of <i>M. catarrhalis</i> are disclosed.</p>		

*(Referred to in PCT Gazette No. 38/1998, Section II) **(Referred to in PCT Gazette No. 42/1998, Section II)

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DESCRIPTIONUSPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALISBACKGROUND OF THE INVENTION**I. Field of the Invention**

5 The present invention relates generally to the fields of microbiology, and clinical bacteriology. More particularly, it concerns sequences of the *uspA1* and *uspA2* genes which encode the proteins UspA1 and UspA2, respectively, both of which encode an epitope reactive with monoclonal antibody (MAb) 17C7 and provide useful epitopes for immunodiagnosis and immunoprophylaxis.

II. Description of Related Art

10 It was previously thought that *Moraxella catarrhalis*, previously known as *Branhamella catarrhalis* or *Neisseria catarrhalis*, was a harmless saprophyte of the upper respiratory tract (Catlin, 1990; Berk, 1990). However, during the previous decade, it has been determined that
15 this organism is an important human pathogen. Indeed, it has been established that this Gram-negative diplococcus is the cause of a number of human infections (Murphy, 1989). *M. catarrhalis* is now known to be the third most common cause of both acute and chronic otitis media (Catlin, 1990; Faden *et al.*, 1990; 1991; Marchant, 1990), the most common disease for which infants and children receive health care according to the 1989 Consensus Report. This
20 organism also causes acute maxillary sinusitis, generalized infections of the lower respiratory tract (Murphy and Loeb, 1989) and is an important cause of bronchopulmonary infections in patients with underlying chronic lung disease and, less frequently, of systemic infections in immunocompromised patients (Melendez and Johnson, 1990; Sarubbi *et al.*, 1990; Schonheyder and Ejlersen, 1989; Wright and Wallace, 1989).

25 The 1989 Consensus Report further concluded that prevention of otitis media is an important health care goal due to both its occurrence in infants and children, as well as certain populations of all age groups. In fact, the total financial burden of otitis media has been estimated to be at least \$2.5 billion annually. Vaccines were identified as the most desired approach to prevent this disease for a number of reasons. For example, it was estimated that if

vaccines could reduce the incidence of otitis media by 30%, then the annual health care savings would be at least \$400 million. However, while some progress has been made in the development of vaccines for 2 of the 3 common otitis media pathogens, *Streptococcus pneumoniae* and *Haemophilus influenzae*, there is no indication that similar progress has been made with respect to *M. catarrhalis*. This is particularly troublesome in that *M. catarrhalis* now accounts for approximately 17-20% of all otitis media infection (Murphy, 1989). In addition, *M. catarrhalis* is also a significant cause of sinusitis (van Cauwenberge *et al.*, 1993) and persistent cough (Gottfarb and Brauner, 1994) in children. In the elderly, it infects patients with predisposing conditions such as chronic obstructive pulmonary disease (COPD) and other chronic cardiopulmonary conditions (Boyle *et al.*, 1991; Davies and Maesen, 1988; Hager *et al.*, 1987).

Despite its recognized virulence potential, little is known about the mechanisms employed by *M. catarrhalis* in the production of disease or about host factors governing immunity to this pathogen. An antibody response to *M. catarrhalis* otitis media has been documented by means of an ELISA system using whole *M. catarrhalis* cells as antigen and acute and convalescent sera or middle ear fluid as the source of antibody (Leinonen *et al.*, 1981). The development of serum bactericidal antibody during *M. catarrhalis* infection in adults was shown to be dependent on the classical complement pathway (Chapman *et al.*, 1985). And more recently, it was reported that young children with *M. catarrhalis* otitis media develop an antibody response in the middle ear but fail to develop a systemic antibody response in a uniform manner (Faden *et al.*, 1992).

Previous attempts have been made to identify and characterize *M. catarrhalis* antigens that would serve as potentially important targets of the human immune response to infection (Murphy, 1989; Goldblatt *et al.*, 1990; Murphy *et al.*, 1990). Generally speaking, the surface of *M. catarrhalis* is composed of outer membrane proteins (OMPs), lipooligosaccharide (LOS) and fimbriae. *M. catarrhalis* appears to be somewhat distinct from other Gram-negative bacteria in that attempts to isolate the outer membrane of this organism using detergent fractionation of cell envelopes has generally proven to be unsuccessful in that the procedures did not yield consistent results (Murphy, 1989; Murphy and Loeb, 1989). Moreover, preparations were found to be contaminated with cytoplasmic membranes, suggesting an unusual characteristic of the *M. catarrhalis* cell envelope.

Passive immunization with polyclonal antisera raised against outer membrane vesicles of the *M. catarrhalis* strain 035E was also found to protect against pulmonary challenge by the heterologous *M. catarrhalis* strain TTA24. In addition, active immunization with *M. catarrhalis* outer membrane vesicles resulted in enhanced clearance of this organism from the lungs after challenge. The positive effect of immunization in pulmonary clearance indicates that antibodies play a major role in immunoprotection from this pathogen. In addition, the protection observed against pulmonary challenge with a heterologous *M. catarrhalis* strain demonstrates that one or more conserved surface antigens are targets for antibodies which function to enhance clearance of *M. catarrhalis* from the lungs.

Outer membrane proteins (OMPs) constitute major antigenic determinants of this unencapsulated organism (Bartos and Murphy, 1988) and different strains share remarkably similar OMP profiles (Bartos and Murphy, 1988; Murphy and Bartos, 1989). At least three different surface-exposed outer membrane antigens have been shown to be well-conserved among *M. catarrhalis* strains; these include the 81 kDa CopB OMP (Helminen *et al.*, 1993b), the heat-modifiable CD OMP (Murphy *et al.*, 1993) and the high-molecular weight UspA antigen (Helminen *et al.*, 1994). Of these three antigens, both the CopB protein and UspA antigen have been shown to bind antibodies which exert biological activity against *M. catarrhalis* in an animal model (Helminen *et al.*, 1994; Murphy *et al.*, 1993).

The MAb, designated 17C7, was described as binding to UspA, a very high molecular weight protein that migrated with an apparent molecular weight (in SDS-PAGE) of at least 250 kDa (Helminen *et al.*, 1994; Klingman and Murphy, 1994). MAb 17C7 enhanced pulmonary clearance of *M. catarrhalis* from the lungs of mice when used in passive immunization studies and, in colony blot radioimmunoassay analysis, bound to every isolate of *M. catarrhalis* examined. This same MAb also reacted, although less intensely, with another antigen band of approximately 100 kDa, as described in U.S. Patent No. 5,552,146 (incorporated herein by reference). A recombinant bacteriophage that contained a fragment of *M. catarrhalis* chromosomal DNA that expressed a protein product that bound MAb 17C7 was also identified and migrated at a rate similar or indistinguishable from that of the native UspA antigen from *M. catarrhalis* (Helminen *et al.*, 1994).

With the rising importance of this pathogen in respiratory tract infections, identification of the surface components of this bacterium involved in virulence expression and immunity is becoming more important. To date, there are no vaccines available, against any other OMP, LOS or fimbriae, that induce protective antibodies against *M. catarrhalis*. Thus, it is clear that there remains a need to identify and characterize useful antigens and which can be employed in the preparation of immunoprophylactic reagents. Additionally, once such an antigen or antigens is identified, there is a need for providing methods and compositions which will allow the preparation of vaccines and in quantities that will allow their use on a wide scale basis in prophylactic protocols.

SUMMARY OF THE INVENTION

It is, therefore, an object of the present invention to provide new UspA1 and UspA2 proteins and genes coding therefor. It also is an object of the present invention to provide methods of using these new proteins, for example, in the preparation of agents for the treatment and inhibition of *M. catarrhalis* infection. It also is contemplated that through the use of other technologies such as antibody treatment and immunoprophylaxis that one can inhibit or even prevent *M. catarrhalis* infections.

In satisfying these goals, there are provided epitopic core sequences of UspA1 and UspA2 which can serve as the basis for the preparation of therapeutic or prophylactic compositions or vaccines which comprise peptides of 7, 10, 20, 30, 40, 50 or even 60 amino acids in length that elicit an antigenic reaction and a pharmaceutically acceptable buffer or diluent. These peptides may be coupled to a carrier, adjuvant, another peptide or other molecule such that an effective antigenic response to *M. catarrhalis* is retained or even enhanced. Alternatively, these peptides may act as carriers themselves when coupled to another peptide or other molecule that elicits an antigenic response to *M. catarrhalis* or another pathogen. For example, UspA2 can serve as a carrier for an oligosaccharide.

In one embodiment, the epitopic core sequences of UspA1 and UspA2 comprise one or more isolated peptides of 7, 10, 20, 30, 40, 50 or even 60 amino acids in length having the amino acid sequence AQQQDQH (SEQ ID NO:17).

In another embodiment, there are provided nucleic acids, *uspA1* and *uspA2*, which encode the UspA1 and the UspA2 antigens, respectively, as well as the amino acid sequences of the UspA1 and UspA2 antigens of the *M. catarrhalis* isolates O35E, TTA24, TTA37, and O46E. It is envisioned that nucleic acid segments and fragments of the genes *uspA1* and *uspA2* and the UspA1 and UspA2 antigens will be of value in the preparation and use of therapeutic or prophylactic compositions or vaccines for treating, inhibiting or even preventing *M. catarrhalis* infections.

In another embodiment, there is provided a method for inducing an immune response in a mammal comprising the step of providing to the mammal an antigenic composition that comprises an isolated peptide of about 20 to about 60 amino acids that contains the identified epitopic core sequence and a pharmaceutically acceptable buffer or diluent.

In another embodiment, there is provided a method for diagnosing *M. catarrhalis* infection which comprises the step of determining the presence, in a sample, of an *M. catarrhalis* amino acid sequence corresponding to residues of the epitopic core sequences of either the UspA1 or UspA2 antigen. This method may comprise PCR™ detection of the nucleotide sequences or alternatively an immunologic reactivity of an antibody to either a UspA1 or UspA2 antigen.

In a further embodiment, there is provided a method for treating an individual having an *M. catarrhalis* infection which comprises providing to the individual an isolated peptide of about 20 to about 60 amino acids that comprises at least about 10 consecutive residues of the amino acid sequence identified as an epitopic core sequence of UspA1 or UspA2.

In a still further embodiment, there is provided a method for preventing or limiting an *M. catarrhalis* infection that comprises providing to a subject an antibody that reacts immunologically with the identified epitopic core region of either UspA1 or UspA2 of *M. catarrhalis*.

In another embodiment, there is provided a method for screening a peptide for reactivity with an antibody that binds immunologically to UspA1, UspA2 or both which comprises the steps of providing the peptide and contacting the peptide with the antibody and then

determining the binding of the antibody to the peptide. This method may comprise an immunoassay such as a western blot, an ELISA, an RIA or an immunoaffinity separation.

In a still further embodiment, there is provided a method for screening a UspA1 or UspA2 peptide for its ability to induce a protective immune response against *M. catarrhalis* by providing the peptide, administering it in a suitable form to an experimental animal, challenging the animal with *M. catarrhalis* and then assaying for an *M. catarrhalis* infection in the animal. It is envisioned that the animal used will be a mouse that is challenged by a pulmonary exposure to *M. catarrhalis* and that the assaying comprises assessing the degree of pulmonary clearance by the mouse.

Other objects, features and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating preferred embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

FIG. 1. Southern blot analysis of *PvuII*-digested chromosomal DNA from strains of *M. catarrhalis* using a probe from the *uspA1* gene. Bacterial strain designations are at the top; kilobase (kb) position markers are on the left.

FIG. 2A. Proteins present in whole cell lysates of the wild-type strain O35E and the isogenic *uspA1* mutant strain. These proteins were resolved by SDS-PAGE and stained with Coomassie blue. The left lane (WT) contains the wild-type strain and right lane (MUT) contains

the mutant. The arrows indicate the protein, approximately 120 kDa in size, that is present in the wild-type and missing in the mutant. Kilodalton position markers are on the left.

FIG. 2B. Western blot analysis of whole cell lysates of the wild-type strain O35E and the isogenic *uspA1* mutant strain. These proteins were resolved by SDS-PAGE and probed with MAb 17C7 in western blot analysis. The left lane (WT) contains the wild-type strain and the right lane (MUT) contains the mutant. Kilodalton position markers are on the left. It can be seen that both strains possess the very high molecular weight band reactive with MAb 17C7 whereas only the wild-type strain also has a band of approximately 120 kDa that binds this MAb.

FIG. 2C. Western blot analysis of whole cell lysate (WCL) and EDTA-extracted outer membrane vesicles (OMV) from the wild-type strain O35E (WT) and the isogenic *uspA1* mutant (MUT) using MAb 17C7. Samples were either heated at 37°C for 15 minutes (H) or at 100°C for 5 minutes (B) prior to SDS-PAGE. Molecular weight position markers (in kilodaltons) are indicated on the left. The open arrow indicates the position of the very high molecular weight form of the MAb 17C7-reactive antigen; the closed arrow indicates the position of the approximately 120 kDa protein; the open circle indicates the position of the approximately 70-80 kDa protein.

FIG. 3. Southern blot analysis of chromosomal DNA from the wild-type *M. catarrhalis* strain O35E and the isogenic *uspA1* mutant. Chromosomal DNA was digested with *PvuII* and probed with a 0.6 kb *BglIII-PvuII* fragment from the *uspA1* gene. The wild-type strain is listed as O35E at the top of this figure and the mutant strain is listed as O35E-*uspA1*⁻. Kilobase position markers are present on the left side.

FIG. 4. Western blot reactivity of proteins in *M. catarrhalis* strain O35E outer membrane vesicles (labeled O35E OMV) and the MF-4-1 GST fusion protein (labeled GST fusion protein) with MAb 17C7.

FIG. 5. PCRTM products obtained by the use of the T3 and P10 primers (middle lane - 0.9 kb product) and the T7 and P9 primers (right lane - 1.7 kb product) when used in a PCRTM

amplification with chromosomal DNA from the *uspA1* mutant. A kb ladder is present in the first lane; several kb position markers are listed on the left side of this figure.

FIG. 6A-6C. SDS-PAGE and westerns of purified proteins. FIG. 6A. Coomassie blue stained gel of purified UspA2 (lane 2). FIG. 6B. Coomassie blue stained gel of purified UspA1 prepared without heating of sample (lane 4), heated for 3 min at 100°C (lane 5), heated for 5 min at 100°C (lane 6), and heated for 10 min at 100°C (lane 7). FIG. 6C. Western of the purified UspA2 (lane 9) and purified UspA1 (lane 10) probed with the 17C7 MAb. Both proteins were heated 10 min. The molecular size markers in lanes 1, 3, and 8 are as indicated in kilodaltons.

FIG. 7. Interaction of purified UspA1 and UspA2 with HEp-2 cells as determined by ELISA. HEp-2 cell monolayers cultured in 96-well plate were incubated with serially diluted UspA1 or UspA2. O35E bacterial strain was used as the positive control. The bacteria were diluted analogous to the proteins beginning with a suspension with an A_{550} of 1.0. The bound proteins or attached bacteria were detected with a 1:1 mixed antisera to UspA1 and UspA2 as described in the methods.

FIG. 8. Interaction with fibronectin and vitronectin determined by dot blot. The bound vitronectin was detected with rabbit polyclonal antibodies, the protein bound to the fibronectin was detected with pooled sera made against the UspA1 and UspA2.

FIG. 9. The levels of antibodies to the protein UspA1, UspA2 and *M. catarrhalis* O35E strain in normal human sera. Data are the \log_{10} transformed end-point titers of the IgG (FIGs. 9A-9C) and IgA (FIGs. 9D-9F) antibodies determined by ELISA. The individual titers were plotted according to age group and the geometric mean titer for each age group linked by a solid line. Sera for the 2-18 month old children were consecutive samples from a group of ten children.

FIG. 10. Subclass distribution of IgG antibodies to UspA1 and UspA2 in normal human sera. FIG. 10A shows titers toward UspA1 and FIG. 10B shows titers to UspA2.

FIG. 11. Relationship of serum IgG titers to UspA1 (FIG. 11A) and UspA2 (FIG. 11B) with the bactericidal titer against the O35E strain determined by logistic regression ($p < 0.05$). The solid line indicates the linear relationship between the IgG titer and bactericidal titer. Broken lines represent the 95 % confidence intervals of the linear fit.

FIG. 12. Schematic drawing showing the relative positions of decapeptides 10-24 within the region of UspA1 and UspA2 which binds to MAb 17C7.

FIG. 13. Western dot blot analysis demonstrating reactivity of decapeptides 10-24 with MAb 17C7.

FIG. 14. Partial restriction enzyme map of the *uspA1* (FIG. 14A) and *uspA2* (FIG. 14B) genes from *M. catarrhalis* strain O35E and the mutated versions of these genes. The shaded boxes indicate the open reading frame of each gene. Relevant restriction sites are indicated. PCRTM primer sites (P1-P6) are indicated by arrows. The DNA fragments containing the partial *uspA1* and *uspA2* open reading frames that were derived from *M. catarrhalis* strain O35E chromosomal DNA by PCRTM and cloned into pBluescriptII SK+ are indicated by black bars. Dotted lines connect corresponding restriction sites on these DNA inserts and the chromosome. Open bars indicate the location of the kanamycin or chloramphenicol cassettes, respectively. The DNA probes specific for *uspA1* or *uspA2* are indicated by the appropriate cross-hatched bars and were amplified by PCRTM from *M. catarrhalis* strain O35E chromosomal DNA by the use of the oligonucleotide primer pairs

P3 (5'-GACGCTCAACAGCACTAATACG-3') (SEQ ID NO:20)/P4
(5'-CCAAGCTGATATCACTACC-3') (SEQ ID NO:21) and
P5 (5'-TCAATGCCTTTGATGGTC-3') (SEQ ID NO:22)/P6
(5'-TGTATGCCGCTACTCGCAGCT-3') (SEQ ID NO:23), respectively.

FIG. 15. Detection of the UspA1 and UspA2 proteins in wild-type and mutant strains of *M. catarrhalis* O35E. Proteins present in EDTA-extracted outer membrane vesicles from the wild-type strain (lane 1), the *uspA1* mutant strain O35E.1 (lane 2), the *uspA2* mutant strain O35E.2 (lane 3), and the isogenic *uspA1 uspA2* double mutant strain O35E.12 (lane 4) were resolved by SDS-PAGE, and either stained with Coomassie blue (FIG. 15A) or transferred to nitrocellulose and probed with MAb 17C7 followed by radioiodinated goat anti-mouse

immunoglobulin in western blot analysis. In FIG. 15A, the closed arrow indicates the very high molecular weight form of the UspA antigen which is comprised of both UspA1 and UspA2. In FIG. 15B, the bracket on the left indicates the very high molecular weight forms of the UspA1 and UspA2 proteins that bind MAb 17C7. The open arrow indicates the 120 kDa, putative monomeric form of UspA1. The closed arrow indicates the 85 kDa, putative monomeric form of UspA2. Molecular weight position markers (in kilodaltons) are present on the left.

FIG. 16. Comparison of the rate and extent of growth of the wild-type and mutant strains of *M. catarrhalis*. The wild-type strain O35E (closed squares), the *uspA1* mutant O35E.1 (open squares), the *uspA2* mutant O35E.2 (closed circles), and the *uspA1 uspA2* double mutant O35E.12 (open circles) of *M. catarrhalis* O35E from overnight broth cultures were diluted to a density of 35 Klett units in BHI broth and subsequently allowed to grow at 37° with shaking. Growth was followed by means of turbidity measurements.

FIG. 17. Susceptibility of wild-type and mutant strains of *M. catarrhalis* to killing by normal human serum. Cells of the wild-type parent strain O35E (diamonds), *uspA1* mutant O35E.1 (triangles), *uspA2* mutant O35E.2 (circles), and *uspA1 uspA2* double mutant O35E.12 (squares) from logarithmic-phase BHI broth cultures were incubated in the presence of 10% (v/v) normal human serum (closed symbols) or heat-inactivated normal human serum (open symbols). Data are presented as the percentage of the original inoculum remaining at each time point.

DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

The present invention relates to the identification of epitopes useful for developing potential vaccines against *M. catarrhalis*. Early work was directed at determining the molecular nature of the UspA antigen and characterize the epitope which is recognized by the MAb 17C7. Preliminary work indicated that MAb 17C7 recognizes a single antigenic epitope and it was believed that this epitope was encoded by a single gene. However, isolation of the protein which contained the epitope yielded unexpected results. MAb 17C7 recognized a single epitope, but the characteristics of the protein associated with the epitope suggested the existence

of not one but two separate proteins. Further careful analyses led to a surprising discovery. A single epitope of the UspA antigen is recognized by the MAb 17C7, but this epitope is present in two different proteins, UspA1 and UspA2, which are encoded by two different genes *uspA1* and *uspA2*, respectively, and only have 43% identity to each other. The present invention provides the nucleotide sequences of the genes *uspA1* and *uspA2*, their respective protein products, UspA1 and UspA2, and the shared epitope recognized by MAb 17C7.

In addition, the present invention provides insights into the antigenic structure of the UspA protein based on the analysis of the sequences of the UspA1 and UspA2 proteins which comprise the protein. Characterization of the epitopic region of the molecule that is targeted by the MAb 17C7 permits the development of agents that will be useful in protecting against *M. catarrhalis* infections, e.g., in the preparation of prophylactic reagents. Particular embodiments relate to the amino acid and nucleic acids corresponding to the UspA1 and UspA2 proteins, peptides and antigenic compositions derived therefrom, and methods for the diagnosis and treatment of *M. catarrhalis* disease.

As stated previously, *M. catarrhalis* infections present a serious health challenge, especially to the young. Thus, there is a clear need to develop compositions and methods that will aid in the treatment and diagnosis of this disease. The present invention, by virtue of new information regarding the structure of the UspA antigen of *M. catarrhalis*, and discovery of the two new and distinct proteins UspA1 and UspA2 provides such improved compositions and methods. UspA1 and UspA2 represent important antigenic determinants, as the MAb 17C7 has been shown to protect experimental animals, as measured in a pulmonary clearance model, when provided in passive immunizations.

In a first embodiment, the present invention provides for the identification of the proteins UspA1 and UspA2 from *M. catarrhalis* strain O35E. The UspA1 protein comprises about 831 amino acid residues and has a predicted mass of about 88,271 daltons (SEQ ID NO:1). The UspA2 protein comprises about 576 residues and has a predicted mass of about 62,483 daltons (SEQ ID NO:3). UspA2 is not a truncated or processed form of UspA1.

In a second embodiment, the present invention has identified the specific epitope to which MAb 17C7 binds. A common peptide sequence, designated as the "3Q" peptide, found between amino acid residues 480-502 and 582-604 of the UspA1 protein (SEQ ID NO:1) and

residues 355-377 of the UspA2 protein (SEQ ID NO:3) of *M. catarrhalis* strain 035E, encompasses the region which appears to be recognized by MAb 17C7. (Note that numbering of the amino acid residues is based upon strain O35E as provided in SEQ ID NO:3.) It is envisioned that this region plays an important role in the biology of the pathogen and, from this information, one will deduce amino acids residues that are critical in MAb 17C7 antibody binding. It also is envisioned that, based upon this information, one will be able to design epitopic regions that have either a higher or lower affinity for the MAb 17C7 or other antibodies. Further embodiments of the present invention are discussed below.

In another preferred embodiment, the present invention provides DNA segments, vectors and the like comprising at least one isolated gene, DNA segment or coding region that encodes a *M. catarrhalis* UspA1 or UspA2 protein, polypeptide, domain, peptide or any fusion protein thereof. Herein are provided at least an isolated gene, DNA segment or coding region that encodes a *M. catarrhalis uspA1* gene comprising about 2493 base pairs (bp) (SEQ ID NO:2) of strain O35E, about 3381 bp (SEQ ID NO:6) of strain O46E, about 3538 bp (SEQ ID NO:10) of strain TTA24, or about 3292 bp (SEQ ID NO:14) of strain TTA37. Further provided are at least an isolated gene, DNA segment or coding region that encodes a *M. catarrhalis uspA2* gene comprising about 1728 bp (SEQ ID NO:4) of strain O35E, about 3295 bp (SEQ ID NO:8) of strain O46E, about 2673 bp (SEQ ID NO:12), or about 4228 bp (SEQ ID NO:16) of strain TTA37. It is envisioned that the *uspA1* and *uspA2* genes will be useful in the preparation of proteins, antibodies, screening assays for potential candidate drugs and the like to treat or inhibit, or even prevent, *M. catarrhalis* infections.

The present invention also provides for the use of the UspA1 or UspA2 proteins or peptides as immunogenic carriers of other agents which are useful for the treatment, inhibition or even prevention of other bacterial, viral or parasitic infections. It is envisioned that either the UspA1 or UspA2 antigen, or portions thereof, will be coupled, bonded, bound, conjugated or chemically-linked to one or more agents via linkers, polylinkers or derivatized amino acids such that a bispecific or multivalent composition or vaccine which is useful for the treatment, inhibition or even prevention of infection by *M. catarrhalis* and another pathogen(s) is prepared. It is further envisioned that the methods used in the preparation of these compositions will be familiar to those of skill in the art and, for example, similar to those used to prepare conjugates to keyhole limpet hemocyanin (KLH) or bovine serum albumin (BSA).

It is important to note that screening methods for diagnosis and prophylaxis are readily available, as set forth below. Thus, the ability to (i) test peptides, mutant peptides and antibodies for their reactivity with each other and (ii) test peptides and antibodies for the ability to prevent infections *in vivo*, provide powerful tools to develop clinically important reagents.

1.0 UspA Proteins, Peptides and Polypeptides

The present invention, in one embodiment, encompasses the two new protein sequences, UspA1 and UspA2, and the peptide sequence AQQQDQH (SEQ ID NO:17) identified as the target epitope of MAb 17C7. In addition, inspection of the amino acid sequences of the UspA1 and UspA2 proteins from four strains of *M. catarrhalis* indicated that each protein contained at least one copy of the peptide YELAQQQDQH (SEQ ID NO:18) which binds Mab 17C7 or, in one instance, a peptide nearly identical and having the amino acid sequence YDLAQQQDQH (SEQ ID NO:19).

The peptide (YELAQQQDQH, SEQ ID NO:18) occurs twice in UspA1 from strain O35E at residues 486-495 and 588-597 (SEQ ID NO:1) and once in UspA2 from strain O35E at residues 358-367 (SEQ ID NO:3). It occurs once in UspA1 from strain TTA24 at residues 497-506 (SEQ ID NO:9) and twice in UspA2 from strain TTA24 at residues 225-234 and 413-422 (SEQ ID NO:11). The peptide YDLAQQQDQH (SEQ ID NO:19) occurs once in UspA1 from strain O46E at residues 448-457 (SEQ ID NO:5) whereas the peptide YELAQQQDQH (SEQ ID NO:18) occurs once in this same protein at residues 649-658 (SEQ ID NO:5). The peptide YELAQQQDQH (SEQ ID NO:18) occurs once in UspA2 from strain O46E at residues 416-425 (SEQ ID NO:7). The peptide YELAQQQDQH (SEQ ID NO:18) occurs twice in UspA1 from strain TTA37 at residues 478-487 and 630-639 (SEQ ID NO:13) and twice in UspA2 from strain TTA37 at residues 522-531 and 681-690 (SEQ ID NO:15).

Also encompassed in the present invention are hybrid molecules containing portions from one UspA protein, for example the UspA1 protein, fused with portions of the other UspA protein, in this example the UspA2 protein, or fused with other proteins which are useful for identification, such as kanamycin-resistance, or other purposes in the screening of potential vaccines or further characterization of the UspA1 and UspA2 proteins. For example, one may fuse residues 1-350 of any UspA1 with residues 351-576 of any UspA2. Alternatively, a fusion could be generated with sequences from three, four or even five peptide regions represented in a

single UspA antigen. Also encompassed are fragments of the disclosed UspA1 and UspA2 molecules, as well as insertion, deletion or replacement mutants in which non-UspA sequences are introduced, UspA sequences are removed, or UspA sequences are replaced with non-UspA sequences, respectively.

5 UspA1 and UspA2 proteins, according to the present invention, may be advantageously cleaved into fragments for use in further structural or functional analysis, or in the generation of reagents such as UspA-related polypeptides and UspA-specific antibodies. This can be accomplished by treating purified or unpurified UspA1 and/or UspA2 with a peptidase such as endoproteinase glu-C (Boehringer, Indianapolis, IN). Treatment with CNBr is another method by
10 which UspA1 and/or UspA2 fragments may be produced from their natural respective proteins. Recombinant techniques also can be used to produce specific fragments of UspA1 or UspA2.

 More subtle modifications and changes may be made in the structure of the encoded UspA1 or UspA2 polypeptides of the present invention and still obtain a molecule that encodes a protein or peptide with characteristics of the natural UspA antigen. The following is a
15 discussion based upon changing the amino acids of a protein to create an equivalent, or even an improved, second-generation molecule. The amino acid changes may be achieved by changing the codons of the DNA sequence, according to the following codon table:

TABLE I

Amino acid names and abbreviations			Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	UGC	UGU					
Aspartic acid	Asp	D	GAC	GAU					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	UUC	UUU					
Glycine	Gly	G	GGA	GGC	GGG	GGU			
Histidine	His	H	CAC	CAU					
Isoleucine	Ile	I	AUA	AUC	AUU				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU	
Methionine	Met	M	AUG						
Asparagine	Asn	N	AAC	AAU					
Proline	Pro	P	CCA	CCC	CCG	CCU			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU	
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU	
Threonine	Thr	T	ACA	ACC	ACG	ACU			
Valine	Val	V	GUA	GUC	GUG	GUU			
Tryptophan	Trp	W	UGG						
Tyrosine	Tyr	Y	UAC	UAU					

It is known that certain amino acids may be substituted for other amino acids in a protein structure in order to modify or improve its antigenic or immunogenic activity (see, *e.g.*, Kyte & Doolittle, 1982; Hopp, U.S. patent 4,554,101, incorporated herein by reference). For example, through the substitution of alternative amino acids, small conformational changes may

be conferred upon a polypeptide which result in increased activity or stability. Alternatively, amino acid substitutions in certain polypeptides may be utilized to provide residues which may then be linked to other molecules to provide peptide-molecule conjugates which retain enough antigenicity of the starting peptide to be useful for other purposes. For example, a selected
5 UspA1 or UspA2 peptide bound to a solid support might be constructed which would have particular advantages in diagnostic embodiments.

The importance of the hydropathic index of amino acids in conferring interactive biological function on a protein has been discussed generally by Kyte & Doolittle (1982), wherein it is found that certain amino acids may be substituted for other amino acids having a
10 similar hydropathic index or core and still retain a similar biological activity. As displayed in Table II below, amino acids are assigned a hydropathic index on the basis of their hydrophobicity and charge characteristics. It is believed that the relative hydropathic character of the amino acid determines the secondary structure of the resultant protein, which in turn defines the interaction of the protein with substrate molecules. Preferred substitutions which
15 result in an antigenically equivalent peptide or protein will generally involve amino acids having index scores within ± 2 units of one another, and more preferably within ± 1 unit, and even more preferably, within ± 0.5 units.

TABLE II

Amino Acid	Hydropathic Index
Isoleucine	4.5
Valine	4.2
Leucine	3.8
Phenylalanine	2.8
Cysteine/cystine	2.5
Methionine	1.9
Alanine	1.8
Glycine	-0.4
Threonine	-0.7

Table II (Continued)

Amino Acid	Hydropathic Index
Tryptophan	-0.9
Serine	-0.8
Tyrosine	-1.3
Proline	-1.6
Histidine	-3.2
Glutamic Acid	-3.5
Glutamine	-3.5
Aspartic Acid	-3.5
Asparagine	-3.5
Lysine	-3.9
Arginine	-4.5

Thus, for example, isoleucine, which has a hydropathic index of +4.5, will preferably be exchanged with an amino acid such as valine (+ 4.2) or leucine (+ 3.8). Alternatively, at the other end of the scale, lysine (- 3.9) will preferably be substituted for arginine (-4.5), and so on.

Substitution of like amino acids may also be made on the basis of hydrophilicity, particularly where the biological functional equivalent protein or peptide thereby created is intended for use in immunological embodiments. U.S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, *i.e.* with an important biological property of the protein.

As detailed in U.S. Patent 4,554,101, each amino acid has also been assigned a hydrophilicity value. These values are detailed below in Table III.

TABLE III

Amino Acid	Hydrophilic Index
arginine	+3.0
lysine	+3.0
aspartate	+3.0 \pm 1
glutamate	+3.0 \pm 1
serine	+0.3
asparagine	+0.2
glutamine	+0.2
glycine	0
threonine	-0.4
alanine	-0.5
histidine	-0.5
proline	-0.5 \pm 1
cysteine	-1.0
methionine	-1.3
valine	-1.5
leucine	-1.8
isoleucine	-1.8
tyrosine	-2.3
phenylalanine	-2.5
tryptophan	-3.4

It is understood that one amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those which are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

Accordingly, these amino acid substitutions are generally based on the relative similarity of R-group substituents, for example, in terms of size, electrophilic character, charge, and the like. In general, preferred substitutions which take various of the foregoing characteristics into

consideration will be known to those of skill in the art and include, for example, the following combinations: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, peptides derived from these polypeptides, including peptides of at least about 6 consecutive amino acids from these sequences, are contemplated. Alternatively, such peptides may comprise about 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59 or 60 consecutive residues. For example, a peptide that comprises 6 consecutive amino acid residues may comprise residues 1 to 6, 2 to 7, 3 to 8 and so on of the UspA1 or UspA2 protein. Such peptides may be represented by the formula

$$x \text{ to } (x + n) = 5' \text{ to } 3' \text{ the positions of the first and last consecutive residues}$$

where x is equal to any number from 1 to the full length of a UspA1 or UspA2 protein and n is equal to the length of the peptide minus 1. So, for UspA1, x = 1 to 831, for UspA2, x = 1 to 576. Where the peptide is 10 residues long (n = 10-1), the formula represents every 10-mer possible for each antigen. For example, where x is equal to 1 the peptide would comprise residues 1 to (1 + [10-1]), or 1 to 10. Where x is equal to 2, the peptide would comprise residues 2 to (2 + [10-2]), or 2 to 11, and so on.

Syntheses of peptides are readily achieved using conventional synthetic techniques such as the solid phase method (e.g., through the use of a commercially available peptide synthesizer such as an Applied Biosystems Model 430A Peptide Synthesizer). Peptides synthesized in this manner may then be aliquoted in predetermined amounts and stored in conventional manners, such as in aqueous solutions or, even more preferably, in a powder or lyophilized state pending use.

In general, due to the relative stability of peptides, they may be readily stored in aqueous solutions for fairly long periods of time if desired, e.g., up to six months or more, in virtually any aqueous solution without appreciable degradation or loss of antigenic activity. However, where extended aqueous storage is contemplated it will generally be desirable to include agents including buffers such as Tris or phosphate buffers to maintain a pH of 7.0 to 7.5. Moreover, it may be desirable to include agents which will inhibit microbial growth, such as sodium azide or

Merthiolate. For extended storage in an aqueous state it will be desirable to store the solutions at 4°C, or more preferably, frozen. Of course, where the peptide(s) are stored in a lyophilized or powdered state, they may be stored virtually indefinitely, *e.g.*, in metered aliquots that may be rehydrated with a predetermined amount of water (preferably distilled, deionized) or buffer prior to use.

Of particular interest are peptides that represent epitopes that lie within the UspA antigen and are encompassed by the UspA1 and UspA2 proteins of the present invention. An "epitope" is a region of a molecule that stimulates a response from a T-cell or B-cell, and hence, elicits an immune response from these cells. An epitopic core sequence, as used herein, is a relatively short stretch of amino acids that is structurally "complementary" to, and therefore will bind to, binding sites on antibodies or T-cell receptors. It will be understood that, in the context of the present disclosure, the term "complementary" refers to amino acids or peptides that exhibit an attractive force towards each other. Thus, certain epitopic core sequences of the present invention may be operationally defined in terms of their ability to compete with or perhaps displace the binding of the corresponding UspA antigen to the corresponding UspA-directed antisera.

The identification of epitopic core sequences is known to those of skill in the art. For example U.S. Patent 4,554,101 teaches identification and preparation of epitopes from amino acid sequences on the basis of hydrophilicity, and by Chou-Fasman analyses. Numerous computer programs are available for use in predicting antigenic portions of proteins, examples of which include those programs based upon Jameson-Wolf analyses (Jameson and Wolf, 1988; Wolf *et al.*, 1988), the program PepPlot® (Brutlag *et al.*, 1990; Weinberger *et al.*, 1985), and other new programs for protein tertiary structure prediction (Fetrow & Bryant, 1993) that can be used in conjunction with computerized peptide sequence analysis programs.

In general, the size of the polypeptide antigen is not believed to be particularly crucial, so long as it is at least large enough to carry the identified core sequence or sequences. The smallest useful core sequence anticipated by the present disclosure would be on the order of about 6 amino acids in length. Thus, this size will generally correspond to the smallest peptide antigens prepared in accordance with the invention. However, the size of the antigen may be larger where desired, so long as it contains a basic epitopic core sequence.

2.0 UspA1 and UspA2 Nucleic Acids

In addition to polypeptides, the present invention also encompasses nucleic acids encoding the UspA1 (SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10 and SEQ ID NO:14) and UspA2 (SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12 and SEQ ID NO:16) proteins from the exemplary *M. catarrhalis* strains O35E, O46E, TTA24 and TTA37, respectively. Because of the degeneracy of the genetic code, many other nucleic acids also may encode a given UspA1 or UspA2 protein. For example, four different three-base codons encode the amino acids alanine, glycine, proline, threonine and valine, while six different codons encode arginine, leucine and serine. Only methionine and tryptophan are encoded by a single codon. Table I provides a list of amino acids and their corresponding codons for use in such embodiments. In order to generate any nucleic acid encoding UspA1 or UspA2, one need only refer to the codon table provided herein. Substitution of the natural codon with any codon encoding the same amino acid will result in a distinct nucleic acid that encodes UspA1 or UspA2. As a practical matter, this can be accomplished by site-directed mutagenesis of an existing *uspA1* or *uspA2* gene or *de novo* chemical synthesis of one or more nucleic acids.

These observations regarding codon selection, site-directed mutagenesis and chemical synthesis apply with equal force to the discussion of substitutional mutant UspA1 or UspA2 peptides and polypeptides, as set forth above. More specifically, substitutional mutants generated by site-directed changes in the nucleic acid sequence that are designed to alter one or more codons of a given polypeptide or epitope may provide a more convenient way of generating large numbers of mutants in a rapid fashion. The nucleic acids of the present invention provide for a simple way to generate fragments (*e.g.*, truncations) of UspA1 or UspA2, UspA1-UspA2 fusion molecules (discussed above) and UspA1 or UspA2 fusions with other molecules. For example, utilization of restriction enzymes and nuclease in the *uspA1* or *uspA2* gene permits one to manipulate the structure of these genes, and the resulting gene products.

The nucleic acid sequence information provided by the present disclosure also allows for the preparation of relatively short DNA (or RNA) sequences that have the ability to specifically hybridize to gene sequences of the selected *uspA1* or *uspA2* gene. In these aspects nucleic acid probes of an appropriate length are prepared based on a consideration of the coding sequence of the *uspA1* or *uspA2* gene, or flanking regions near the *uspA1* or *uspA2* gene, such as regions downstream and upstream in the *M. catarrhalis* chromosome. The ability of such

nucleic acid probes to specifically hybridize to either *uspA1* or *uspA2* gene sequences lends them particular utility in a variety of embodiments. For example, the probes can be used in a variety of diagnostic assays for detecting the presence of pathogenic organisms in a given sample. In addition, these oligonucleotides can be inserted, in frame, into expression constructs for the purpose of screening the corresponding peptides for reactivity with existing antibodies or for the ability to generate diagnostic or therapeutic reagents.

To provide certain of the advantages in accordance with the invention, the preferred nucleic acid sequence employed for hybridization studies or assays includes sequences that are complementary to at least a 10 to 20, or so, nucleotide stretch of the sequence, although sequences of 30 to 60 or so nucleotides are also envisioned to be useful. A size of at least 9 nucleotides in length helps to ensure that the fragment will be of sufficient length to form a duplex molecule that is both stable and selective. Though molecules having complementary sequences over stretches greater than 10 bases in length are generally preferred, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of the specific hybrid molecules obtained. Thus, one will generally prefer to design nucleic acid molecules having either *uspA1* or *uspA2* gene-complementary stretches of 15 to 20 nucleotides, or even longer, such as 30 to 60, where desired. Such fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, by application of nucleic acid reproduction technology, such as the PCR™ technology of U.S. Patent 4,603,102, or by introducing selected sequences into recombinant vectors for recombinant production.

The probes that would be useful may be derived from any portion of the sequences of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16. Therefore, probes are specifically contemplated that comprise nucleotides 1 to 9, or 2 to 10, or 3 to 11 and so forth up to a probe comprising the last 9 nucleotides of the nucleotide sequence of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16. Thus, each probe would comprise at least about 9 linear nucleotides of the nucleotide sequence of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16., designated by the formula " n to $n + 8$," where n is an integer from 1 to the number of nucleotides in the sequence. Longer probes that hybridize to the *uspA1* or *uspA2* gene under low, medium, medium-high and high stringency conditions are

also contemplated, including those that comprise the entire nucleotide sequence of SEQ ID NO:2 or SEQ ID NO:4 or SEQ ID NO:6 or SEQ ID NO:8 or SEQ ID NO:10 or SEQ ID NO:12 or SEQ ID NO:14 or SEQ ID NO:16. This hypothetical may be repeated for probes having lengths of about 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100 and greater bases.

In that the UspA antigenic epitopes of the present invention are believed to be indicative of pathogenic *Moraxella* species as exemplified by strains O35E, O46E, TTA24 and TTA37, the probes of the present invention will find particular utility as the basis for diagnostic hybridization assays for detecting UspA1 or UspA2 DNA in clinical samples. Exemplary clinical samples that can be used in the diagnosis of infections are thus any samples which could possibly include *Moraxella* nucleic acid, including middle ear fluid, sputum, mucus, bronchoalveolar fluid, amniotic fluid or the like. A variety of hybridization techniques and systems are known which can be used in connection with the hybridization aspects of the invention, including diagnostic assays such as those described in Falkow *et al.*, U.S. Patent 4,358,535. Depending on the application envisioned, one will desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of the probe toward the target sequence. For applications requiring a high degree of selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, for example, one will select relatively low salt and/or high temperature conditions, such as provided by 0.02M-0.15M NaCl at temperatures of 50°C to 70°C. These conditions are particularly selective, and tolerate little, if any, mismatch between the probe and the template or target strand.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent hybridization conditions are called for in order to allow formation of the heteroduplex. In these circumstances, one would desire to employ conditions such as 0.15M-0.9M salt, at temperatures ranging from 20°C to 55°C. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and the method of choice will generally depend on the desired results.

In certain embodiments, one may desire to employ nucleic acid probes to isolate variants from clone banks containing mutated clones. In particular embodiments, mutant clone colonies growing on solid media which contain variants of the *UspA1* and/or *UspA2* sequence could be identified on duplicate filters using hybridization conditions and methods, such as those used in colony blot assays, to obtain hybridization only between probes containing sequence variants and nucleic acid sequence variants contained in specific colonies. In this manner, small hybridization probes containing short variant sequences of either the *uspA1* or *uspA2* gene may be utilized to identify those clones growing on solid media which contain sequence variants of the entire *uspA1* or *uspA2* gene. These clones can then be grown to obtain desired quantities of the variant *UspA1* or *UspA2* nucleic acid sequences or the corresponding *UspA* antigen.

In clinical diagnostic embodiments, nucleic acid sequences of the present invention are used in combination with an appropriate means, such as a label, for determining hybridization. A wide variety of appropriate indicator means are known in the art, including radioactive, enzymatic or other ligands, such as avidin/biotin, which are capable of giving a detectable signal. In preferred diagnostic embodiments, one will likely desire to employ an enzyme tag such as urease, alkaline phosphatase or peroxidase, instead of radioactive or other environmental undesirable reagents. In the case of enzyme tags, colorimetric indicator substrates are known which can be employed to provide a means visible to the human eye or spectrophotometrically, to identify specific hybridization with pathogen nucleic acid-containing samples.

In general, it is envisioned that the hybridization probes described herein will be useful both as reagents in solution hybridizations as well as in embodiments employing a solid phase. In embodiments involving a solid phase, the test DNA (or RNA) from suspected clinical samples, such as exudates, body fluids (e.g., amniotic fluid, middle ear effusion, bronchoalveolar lavage fluid) or even tissues, is adsorbed or otherwise affixed to a selected matrix or surface. This fixed, single-stranded nucleic acid is then subjected to specific hybridization with selected probes under desired conditions. The selected conditions will depend on the particular circumstances based on the particular criteria required (depending, for example, on the G+C contents, type of target nucleic acid, source of nucleic acid, size of hybridization probe, etc.). Following washing of the hybridized surface so as to remove

nonspecifically bound probe molecules, specific hybridization is detected, or even quantified, by means of the label.

The nucleic acid sequences which encode for the UspA1 and/or UspA2 epitopes, or their variants, may be useful in conjunction with PCRTM methodology to detect *M. catarrhalis*. In general, by applying the PCRTM technology as set out, *e.g.*, in U.S. Patent 4,603,102, one may utilize various portions of either the *uspA1* or *uspA2* sequence as oligonucleotide probes for the PCRTM amplification of a defined portion of a *uspA1* or *uspA2* nucleic acid in a sample. The amplified portion of the *uspA1* or *uspA2* sequence may then be detected by hybridization with a hybridization probe containing a complementary sequence. In this manner, extremely small concentrations of *M. catarrhalis* nucleic acid may be detected in a sample utilizing *uspA1* or *uspA2* sequences.

3.0 Vectors, Host Cells and Cultures for Producing UspA1 and/or UspA2 Antigens

In order to express a UspA1 and/or UspA2 polypeptide, it is necessary to provide an *uspA1* and/or *uspA2* gene in an expression cassette. The expression cassette contains a UspA1 and/or UspA2-encoding nucleic acid under transcriptional control of a promoter. A "promoter" refers to a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a gene. The phrase "under transcriptional control" means that the promoter is in the correct location and orientation in relation to the nucleic acid to control RNA polymerase initiation and expression of the gene. Those promoters most commonly used in prokaryotic recombinant DNA construction include the B-lactamase (penicillinase) and lactose promoter systems (Chang *et al.*, 1978; Itakura *et al.*, 1977; Goeddel *et al.*, 1979) and a tryptophan (*trp*) promoter system (Goeddel *et al.*, 1980; EPO Appl. Publ. No. 0036776). While these are the most commonly used, other microbial promoters have been discovered and utilized, and details concerning their nucleotide sequences have been published, enabling a skilled worker to ligate them functionally with plasmid vectors (EPO Appl. Publ. No. 0036776). Additional examples of useful promoters are provided in Table IV below.

TABLE IV

Promoters	References
Immunoglobulin Heavy Chain	Hanerji <i>et al.</i> , 1983; Gilles <i>et al.</i> , 1983; Grosschedl and Baltimore, 1985; Atchinson and Perry, 1986, 1987; Imler <i>et al.</i> , 1987; Weinberger <i>et al.</i> , 1988; Kiledjian <i>et al.</i> , 1988; Porton <i>et al.</i> , 1990
Immunoglobulin Light Chain	Queen and Baltimore, 1983; Picard and Schaffner, 1984
T-Cell Receptor	Luria <i>et al.</i> , 1987, Winoto and Baltimore, 1989; Redondo <i>et al.</i> , 1990
HLA DQ α and DQ β	Sullivan and Peterlin, 1987
β -Interferon	Goodbourn <i>et al.</i> , 1986; Fujita <i>et al.</i> , 1987; Goodbourn and Maniatis, 1985
Interleukin-2	Greene <i>et al.</i> , 1989
Interleukin-2 Receptor	Greene <i>et al.</i> , 1989; Lin <i>et al.</i> , 1990
MHC Class II 5	Koch <i>et al.</i> , 1989
MHC Class II HLA-DRA	Sherman <i>et al.</i> , 1989
β -Actin	Kawamoto <i>et al.</i> , 1988; Ng <i>et al.</i> , 1989
Muscle Creatine Kinase	Jaynes <i>et al.</i> , 1988; Horlick and Benfield, 1989; Johnson <i>et al.</i> , 1989a
Prealbumin (Transthyretin)	Costa <i>et al.</i> , 1988
Elastase I	Omitz <i>et al.</i> , 1987
Metallothionein	Karin <i>et al.</i> , 1987; Culotta and Hamer, 1989
Collagenase	Pinkert <i>et al.</i> , 1987; Angel <i>et al.</i> , 1987
Albumin Gene	Pinkert <i>et al.</i> , 1987, Tronche <i>et al.</i> , 1989, 1990

TABLE IV (Continued)

Promoters	References
α -Fetoprotein	Godbout <i>et al.</i> , 1988; Campere and Tilghman, 1989
t-Globin	Bodine and Ley, 1987; Perez-Stable and Constantini, 1990
β -Globin	Trudel and Constantini, 1987
e-fos	Cohen <i>et al.</i> , 1987
c-HA-ras	Triesman, 1986; Deschamps <i>et al.</i> , 1985
Insulin	Edlund <i>et al.</i> , 1985
Neural Cell Adhesion Molecule (NCAM)	Hirsch <i>et al.</i> , 1990
α_1 -Antitrypsin	Latimer <i>et al.</i> , 1990
H2B (TH2B) Histone	Hwang <i>et al.</i> , 1990
Mouse or Type I Collagen	Ripe <i>et al.</i> , 1989
Glucose-Regulated Proteins (GRP94 and GRP78)	Chang <i>et al.</i> , 1989
Rat Growth Hormone	Larsen <i>et al.</i> , 1986
Human Serum Amyloid A (SAA)	Edbrooke <i>et al.</i> , 1989
Troponin I (TN I)	Yutzey <i>et al.</i> , 1989
Platelet-Derived Growth Factor	Pech <i>et al.</i> , 1989
Duchenne Muscular Dystrophy	Klamut <i>et al.</i> , 1990
SV40	Banerji <i>et al.</i> , 1981; Moreau <i>et al.</i> , 1981; Sleight and Lockett, 1985; Firak and Subramanian, 1986; Herr and Clarke, 1986; Imbra and Karin, 1986; Kadesch and Berg, 1986; Wang and Calame, 1986; Ondek <i>et al.</i> , 1987; Kuhl <i>et al.</i> , 1987; Schaffner <i>et al.</i> , 1988

TABLE IV (Continued)

Promoters	References
Polyoma	Swartzendruber and Lehman, 1975; Vasseur <i>et al.</i> , 1980; Katinka <i>et al.</i> , 1980, 1981; Tyndell <i>et al.</i> , 1981; Dandolo <i>et al.</i> , 1983; deVilliers <i>et al.</i> , 1984; Hen <i>et al.</i> , 1986; Satake <i>et al.</i> , 1988; Campbell and Villarreal, 1988
Retroviruses	Kriegler and Botchan, 1982, 1983; Levinson <i>et al.</i> , 1982; Kriegler <i>et al.</i> , 1983, 1984a,b, 1988; Bosze <i>et al.</i> , 1986; Miksicek <i>et al.</i> , 1986; Celander and Haseltine, 1987; Thiesen <i>et al.</i> , 1988; Celander <i>et al.</i> , 1988; Chol <i>et al.</i> , 1988; Reisman and Rotter, 1989
Papilloma Virus	Campo <i>et al.</i> , 1983; Lusky <i>et al.</i> , 1983; Spandidos and Wilkie, 1983; Spalholz <i>et al.</i> , 1985; Lusky and Botchan, 1986; Cripe <i>et al.</i> , 1987; Gloss <i>et al.</i> , 1987; Hirochika <i>et al.</i> , 1987, Stephens and Hentschel, 1987; Glue <i>et al.</i> , 1988
Hepatitis B Virus	Bulla and Siddiqui, 1986; Jameel and Siddiqui, 1986; Shaul and Ben-Levy, 1987; Spandau and Lee, 1988; Vannice and Levinson, 1988
Human Immunodeficiency Virus	Muesing <i>et al.</i> , 1987; Hauber and Cullan, 1988; Jakobovits <i>et al.</i> , 1988; Feng and Holland, 1988; Takebe <i>et al.</i> , 1988; Rowen <i>et al.</i> , 1988; Berkhout <i>et al.</i> , 1989; Laspia <i>et al.</i> , 1989; Sharp and Marciniak, 1989; Braddock <i>et al.</i> , 1989
Cytomegalovirus	Weber <i>et al.</i> , 1984; Boshart <i>et al.</i> , 1985; Foecking and Hofstetter, 1986
Gibbon Ape Leukemia Virus	Holbrook <i>et al.</i> , 1987; Quinn <i>et al.</i> , 1989

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